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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 11:09:47 ; Search time 97 Seconds
(without alignments)
5337.827 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933
Sequence: 1 atgggtggtgaggttattc.....tggtttctagctcatcatg 933

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
2	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
3	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
4	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
5	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
6	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
7	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
8	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
9	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
10	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
11	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
12	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
13	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
14	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
15	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
16	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
17	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
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19	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
20	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
21	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
22	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
23	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
24	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
25	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
26	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App
27	831.8	89.2	879	4	US-09-439-313-531 Sequence 531, App

ALIGNMENTS

RESULT 1

US-09-439-313-531

; Sequence 531, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, David C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqiu

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 531

; LENGTH: 879

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-439-313-531

Query Match 89.2%; Score 831.8; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 4.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGGAGCGGCAAGACGCGGGGCACTTCTGGAGACCAACGACTCTCTGTGAA	158
DB	42	CAGGGGGAGCGGCAAGACGCGGGGCACTTCTGGAGACCAACGACTCTCTGTGAA	101
QY	159	GACGCTTGGGAGCAAGAGGTGCAAGTGTGTGTCACCTGCTTCCCTCTGTCAGGGGAG	218
DB	102	GACGCTTGGGAGCAAGAGGTGCAAGTGTGTGTCACCTGCTTCCCTCTGTCAGGGGAG	161
QY	219	CGGCAAGACCAAGCGTGGGCGCTTGGGGAGATACGATGACAGCGGCTTCATGGATCCAG	278
DB	162	CGGCAAGACCAAGCGTGGGCGCTTGGGGAGATACGATGACAGCGGCTTCATGGATCCAG	221
QY	279	GTACCACCTCCATGAGAGATCTGGACAAGTCCACAGAGTCTGCTGGGTAAAGT	338
DB	222	GTACCACCTCCATGAGAGATCTGGACAAGTCCACAGAGTCTGCTGGGTAAAGT	281
QY	339	CCCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGGACAACA	398

282	CCCAGAAAGGATCTCATCGTCTGCTCAGGGACACGGATGTGAACAAGAGGGACAAGCA	341
399	AAAGGAGACTGCTCTACATCTGGCCTTCGCCAATGGGAATTCAGAAAGTAGTAAAACTCGT	458
342	AAAGGGNCTGCTCTACATCTGGCCTTCGCCAATGGGAATTCAGAAAGTAGTAAAACTCGT	401
459	GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAACAAAAAGAGACGACGTCTGACAAA	518
402	GCTGGACAGACGATGTCAACTTAATGTCCTTGACAAACAAAAAGAGACGACGTCTGACAAA	466
519	GGCGGTCAATGCCAGAGAGATGAATGTGGGTAAATGTTGCTGGAAACATGGCACATGATCC	578
462	GGCGGTCAATGCCAGAGAGATGAATGTGGGTAAATGTTGCTGGAAACATGGCACATGATCC	521
579	AAATATTTCCAGATCAGTATGGAATACCACTCTACACTATGCTGTCTCAATGAAGATAA	638
522	AAATATTTCCAGATCAGTATGGAATACCACTCTACACTATGCTGTCTCAATGAAGATAA	581
639	ATTAATGGCCAAACGACTGCTCTATACGGTGTGTATCGAATCAAAAACCAAGCATGG	698
582	ATTAATGGCCAAACGACTGCTCTATACGGTGTGTATCGAATCAAAAACCAAGCATGG	641
699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAAATTTTAAAT	758
642	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAAATTTTAAAT	701
759	CAAGAAAAACGGAAATTTAAATGGCTGGATAGATATGGAAGAACTGTGCTCTCATCTTGC	818
702	CAAGAAAAACGGAAATTTAAATGGCTGGATAGATATGGAAGAACTGTGCTCTCATCTTGC	761
819	TGTAATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGACAAAAATGTTGATGTATC	878
762	TGTAATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGACAAAAATGTTGATGTATC	821
879	TTCTCAAGATCTGGAAGACGGCCAGAGATATGCTGTTTCTTAGTCATCATCATG	933
822	TTCTCAAGATCTGGAAGACGGCCAGAGATATGCTGTTTCTTAGTCATCATCATG	876

RESULT 2

US-09-636-215-531
; Sequence 531, Application US/09636215
; Patent No. 6620922

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/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitchem, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hegler, William
/ TITLE OF INVENTION: COMPOSITIONS OF MATTER
/ TITLE OF INVENTION: DIAGNOSIS OF
/ FILE REFERENCE: 210121.42171C17
/ CURRENT APPLICATION NUMBER: US/0
/ CURRENT FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: Fast-SEQ for Windows V
/ SEQ ID NO 531
/ LENGTH: 879
/ TYPE: DNA
/ ORGANISM: Homo sapiens

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US-09-636-215-531

Query Match 89.2%; Score 831.8; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. No. 4.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0

99	QY	CAGGGGAGCGGCAAGAGCAACGTGGGCACTCTCGGAGACCACAAACGACTCCTCTGTGAA	158
42	Db	CAGGGGAGCGGCAAGAGCAACGTGGGCACTCTCGGAGACCACAAACGACTCCTCTGTGAA	101
159	QY	GAGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGTCGCCACTGCTTCCCTCTGCTGCAGGGGGAG	218
102	Db	GAGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGTCGCCACTGCTTCCCTCTGCTGCAGGGGGAG	161
219	QY	CGGCAAGAGCAACGTGGGCGCTTTGGGAGACATACGATGACAGCGCCTTCATGATCCAG	278
162	Db	CGGCAAGAGCAACGTGGTGGGAGACATACGATGACAGCGCCTTCATGATCCAG	221
279	QY	GTACCAAGTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCCCTGGGTGGGTAAAGT	338
222	Db	GTACCAAGTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCCCTGGGTGGGTAAAGT	281
339	QY	CCCCAGAAAGGATCTCATCGTCAATGCTCAGGAGCACTGATGTGAACAGAGGGGCAAGCA	398
282	Db	CCCCAGAAAGGATCTCATCGTCAATGCTCAGGAGCACTGATGTGAACAGAGGGGCAAGCA	341
399	QY	AAAGAGACTGCTCTACATCTGGGCTCTGGCCMAATGGGAATTCAGAAGTAGTAAACCTCGT	458
342	Db	AAAGAGACTGCTCTACATCTGGGCTCTGGCCMAATGGGAATTCAGAAGTAGTAAACCTCGT	401
459	QY	GCTGGACAGACGATGTCACACTTAATGCTCTGACAAACAAAGAGGAGCAGCTCTGCACAA	518
402	Db	GCTGGACAGACGATGTCACACTTAATGCTCTGACAAACAAAGAGGAGCAGCTCTGCACAA	461
519	QY	GGCCGTAACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACAATGGCACTGATCC	578
462	Db	GGCCGTAACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACAATGGCACTGATCC	521
579	QY	AAATATTCAGATGAGTATGGAATAACCACTCTACACTATGCTGCTCTACAAATGAAGTAA	638
522	Db	AAATATTCAGATGAGTATGGAATAACCACTCTACACTATGCTGCTCTACAAATGAAGTAA	581
639	QY	ATTAAATGCCAAAGCACTGCTCTTATACGGTGCTCATATCGAATCAAAAACAAGCATGG	698
582	Db	ATTAAATGCCAAAGCACTGCTCTTATACGGTGCTCATATCGAATCAAAAACAAGCATGG	641
699	QY	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTTAAT	758
642	Db	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTTAAT	701
759	QY	CAAGAAAAAGCGAAATTTAAATGCGCTGATAGATATGGAAGACTGCTCTCATACTGC	818
702	Db	CAAGAAAAAGCGAAATTTAAATGCGCTGATAGATATGGAAGACTGCTCTCATACTGC	761
819	QY	TGATATGTTGGATCAGCAAGTATAGTCAGGCCCTCTACTTGGACAAAATGTTGATGATC	878
762	Db	TGATATGTTGGATCAGCAAGTATAGTCAGGCCCTCTACTTGGACAAAATGTTGATGATC	821
879	QY	TTCTCAAGATCTCGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG	933
822	Db	TTCTCAAGATCTCGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG	876

RESULT 3

RESOL 3
US-09-685-166A-531
Sequence 531, Application US/09685166A
Patent No. 630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi

QY 579 AAATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 638
 Db 522 AAATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 581
 QY 639 AATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 698
 Db 582 AATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 641
 QY 699 CTTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 758
 Db 642 CTTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 701
 QY 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGATGCTGTCTCAATGAAGATAA 818
 Db 702 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGATGCTGTCTCAATGAAGATAA 761
 QY 819 TGTATGTTGGATCAGCAAGTATGCTGTCTCAATGAAGATGCTGTCTCAATGAAGATAA 878
 Db 762 TGTATGTTGGATCAGCAAGTATGCTGTCTCAATGAAGATGCTGTCTCAATGAAGATAA 821
 QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 933
 Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 876

RESULT 5

US-09-439-313-530
 ; Sequence 530, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yuqui
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.42769
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 530
 ; LENGTH: 1852
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-439-313-530

Query Match 89.2%; Score 831.8; DB 4; Length 1852;
 Best Local Similarity 99.8%; Pred. No. 6.7e-238;
 Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 99 CAGGGGAGCGGCAAGACGACGCTTCTGGAGACCAAGACGCTCTCTGTGAA 158
 Db 771 CAGGGGAGCGGCAAGACGACGCTTCTGGAGACCAAGACGCTCTCTGTGAA 830
 QY 159 GACGCTTGGAGCAAGAGTGCAGAGTGCCTCCCTGCTGAGGGGAG 218
 Db 831 GACGCTTGGAGCAAGAGTGCAGAGTGCCTCCCTGCTGAGGGGAG 890
 QY 219 CGGCAAGCAAGCTGGCGCTTGGGAGACTACGATGACAGGCGCTTCTGATGCCAG 278
 Db 891 CGGCAAGCAAGCTGGCGCTTGGGAGACTACGATGACAGGCGCTTCTGATGCCAG 950
 QY 279 GTACACGCTCCATGGAGAAATTCGACAGCTCCACAGAGCTGCTGTGGGGTAAAGT 338
 Db 951 GTACACGCTCCATGGAGAAATTCGACAGCTCCACAGAGCTGCTGTGGGGTAAAGT 1010

QY 339 CCCAGAAAAGGATCTCATGCTCATGCTCAGGACACGTATGTGAAACAAGAGGACAGCA 398
 Db 1011 CCCAGAAAAGGATCTCATGCTCATGCTCAGGACACGTATGTGAAACAAGAGGACAGCA 1070
 QY 399 AAAGAGACTGCTTACATCTGSCCTCTGCCAATGGGAATTCAGAACTAGTAACTCGT 458
 Db 1071 AAAGAGACTGCTTACATCTGSCCTCTGCCAATGGGAATTCAGAACTAGTAACTCGT 1130
 QY 459 GCTGGACAGAGATGTCAACTTAAATGCTTGAACAACAAAAAGAGGACAGCTCTGACAAA 518
 Db 1131 GCTGGACAGAGATGTCAACTTAAATGCTTGAACAACAAAAAGAGGACAGCTCTGACAAA 1190
 QY 519 GCGCGTACAAATGCCAGGAAGATGAATGTGCGTTAAATGCTTGAACAACAAAAAGAGGACAGCTCTGACAAA 578
 Db 1191 GCGCGTACAAATGCCAGGAAGATGAATGTGCGTTAAATGCTTGAACAACAAAAAGAGGACAGCTCTGACAAA 1250
 QY 579 AAATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 638
 Db 1251 AAATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 1310
 QY 639 AATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 698
 Db 1311 AATATTCAGATGAGTATGGAATACCACTACATGCTGTCTCAATGAAGATAA 1370
 QY 699 CCTCACACCACTGCTTACTTGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 758
 Db 1371 CCTCACACCACTGCTTACTTGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 1430
 QY 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGATGCTGTCTCAATGAAGATAA 818
 Db 1431 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGATGCTGTCTCAATGAAGATAA 1490
 QY 819 TGTATGTTGGATCAGCAAGTATGCTGTCTCAATGAAGATGCTGTCTCAATGAAGATAA 878
 Db 1491 TGTATGTTGGATCAGCAAGTATGCTGTCTCAATGAAGATGCTGTCTCAATGAAGATAA 1550
 QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 933
 Db 1551 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTCTCAATGAAGATAA 1605

RESULT 6

US-09-636-215-530
 ; Sequence 530, Application US/09636215
 ; Patent No. 6620922
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Solk, John H.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Vasil A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.42717C17
 ; CURRENT APPLICATION NUMBER: US/09/636,215
 ; CURRENT FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 852
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 530
 ; LENGTH: 1852


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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-530

Query Match      89.2%; Score 831.8; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 6.7e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 158
DB 771 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 830
QY 159 GACGCTTTGGGAGCAAGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
DB 831 GACGCTTTGGGAGCAAGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 890
QY 219 CGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 278
DB 891 CGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 950
QY 279 GTACCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 338
DB 951 GTACCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 1010
QY 339 CCCGAGAAAGAGTCTCATCTGCTCAGGAGCACTGATGTGAAACAAGAGGAGCAAGCA 398
DB 1011 CCCGAGAAAGAGTCTCATCTGCTCAGGAGCACTGATGTGAAACAAGAGGAGCAAGCA 1070
QY 399 AAAGAGGAGTCTCTACATCTGGGCTCTGCGCAAGCTTCCCAAGAGTTCAGAACTGATCC 458
DB 1071 AAAGAGGAGTCTCTACATCTGGGCTCTGCGCAAGCTTCCCAAGAGTTCAGAACTGATCC 1130
QY 459 GCTGGACAGCAAGTCTCACTTAATGCTTGGACCAACAAGAGGAGCAAGTCTGACAAA 518
DB 1131 GCTGGACAGCAAGTCTCACTTAATGCTTGGACCAACAAGAGGAGCAAGTCTGACAAA 1190
QY 519 GCGCGTACAAATCCAGGAGAGTGAATGCGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 578
DB 1191 GCGCGTACAAATCCAGGAGAGTGAATGCGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1250
QY 579 AAATATCCAGATGATGGAATACCACTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
DB 1251 AAATATCCAGATGATGGAATACCACTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1310
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 698
DB 1311 ATTAATGGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 1370
QY 699 CCTCACACCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 758
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RESULT 7
US-09-685-166A-530
; Sequence 530, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-530

Query Match      89.2%; Score 831.8; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 6.7e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 158
DB 771 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 830
QY 159 GACGCTTTGGGAGCAAGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
DB 831 GACGCTTTGGGAGCAAGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 890
QY 219 CGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 278
DB 891 CGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 950
QY 279 GTACCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 338
DB 951 GTACCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCCTCTGTGAA 1010
QY 339 CCCGAGAAAGAGTCTCATCTGCTCAGGAGCACTGATGTGAAACAAGAGGAGCAAGCA 398
DB 1011 CCCGAGAAAGAGTCTCATCTGCTCAGGAGCACTGATGTGAAACAAGAGGAGCAAGCA 1070
QY 399 AAAGAGGAGTCTCTACATCTGGGCTCTGCGCAAGCTTCCCAAGAGTTCAGAACTGATCC 458
DB 1071 AAAGAGGAGTCTCTACATCTGGGCTCTGCGCAAGCTTCCCAAGAGTTCAGAACTGATCC 1130
QY 459 GCTGGACAGCAAGTCTCACTTAATGCTTGGACCAACAAGAGGAGCAAGTCTGACAAA 518
DB 1131 GCTGGACAGCAAGTCTCACTTAATGCTTGGACCAACAAGAGGAGCAAGTCTGACAAA 1190
QY 519 GCGCGTACAAATCCAGGAGAGTGAATGCGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 578
DB 1191 GCGCGTACAAATCCAGGAGAGTGAATGCGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1250
QY 579 AAATATCCAGATGATGGAATACCACTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
DB 1251 AAATATCCAGATGATGGAATACCACTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1310
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 698
DB 1311 ATTAATGGCCAAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 1370
QY 699 CCTCACACCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAGCATGG 758
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Db 1371 CCTCACCACTGCTACTTGGTATACATGAGCAAAACACAGCAAGTGGTGAATTTTAAT 1430
QY 759 CAGAAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTGC 818
Db 1431 CAAGAAAAAGCGAATTTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATATTGC 1490
QY 819 TGTATGTTGGATCAGCAAGTATAGTACGCTCTACTTTGACAAATGTTGATGATC 878
Db 1491 TGTATGTTGGATCAGCAAGTATAGTACGCTCTACTTTGACAAATGTTGATGATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTATCATCATG 1605

RESULT 8

US-09-429-755-313
; Sequence 313, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-429-755-313

Query Match 89.2%; Score 831.8; DB 4; Length 1852;

Best Local Similarity 99.8%; Pred. No. 6.7e-238;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGCCACAAAGACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGCCACAAAGACTCTCTGTGAA 830
QY 159 GACGCTTGGGAGCAAGAGTGGTGGTCTGCTGCTTCCCTGCTGCGAGGGGAG 218
Db 831 GACGCTTGGGAGCAAGAGTGGTGGTCTGCTGCTTCCCTGCTGCGAGGGGAG 890
QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCAAGATCCCAG 278
Db 891 CGGCAAGAGCAAGTGGTGGGAGACTACGATGACAGCGCTTCAAGATCCCAG 950
QY 279 GTACCACTCCATGGAAGATCTGGAAGCTCCACAGAGTCCGCTGGTGGGTTAACT 338
Db 951 GTACCACTCCATGGAAGATCTGGAAGCTCCACAGAGTCCGCTGGTGGGTTAACT 1010
QY 339 CCCAGAAAGATCTCATGCTATGCTCAGGGAACATGATGTGAAACAAGAGGACAAGCA 398
Db 1011 CCCAGAAAGATCTCATGCTATGCTCAGGGAACATGATGTGAAACAAGAGGACAAGCA 1070
QY 399 AAGAGAGACTGCTCTACATCTGCGCTTCCATGGGAATTCAGAGTAGTAACTCGT 458
Db 1071 AAGAGAGACTGCTCTACATCTGCGCTTCCATGGGAATTCAGAGTAGTAACTCGT 1130
QY 459 GCTGGACAGACGATGCTCAACTTAATGCTTGTGAACAACAAAGAGGACAGCTTGACAAA 518
Db 1131 GCTGGACAGACGATGCTCAACTTAATGCTTGTGAACAACAAAGAGGACAGCTTGACAAA 1190
QY 519 GGGCGTACATGCCAGAGATGAATGGGTTAATGCTGGACATGGCACTGATCC 578

Db 1191 GGCGGTACAATGCCAGGAGATGAATGCGTTAATGTTGCTGGAACATGGCACTGATCC 1250
QY 579 AAATATTCAGATGATGGAATACCACTCTACACTATGCTGCTACAAATGAAGATAA 638
Db 1251 AAATATTCAGATGATGGAATACCACTCTACACTATGCTGCTACAAATGAAGATAA 1310
QY 639 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCATGG 698
Db 1311 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCATGG 1370
QY 699 COTCACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAT 758
Db 1371 COTCACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAT 1430
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 818
Db 1431 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTGC 1490
QY 819 TGTATGTTGGATCAGCAAGTATAGTACGCTCTACTTTCAGCAAAATGTTGATGATC 878
Db 1491 TGTATGTTGGATCAGCAAGTATAGTACGCTCTACTTTCAGCAAAATGTTGATGATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGCTGTTTCTAGTATCATCATG 1605

RESULT 9

US-08-991-789A-291/c
; Sequence 291, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 291:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-08-991-789A-291

Query Match

Best Local Similarity 87.9%; Score 819.8; DB 3; Length 1851;

Matches 832; Conservative 0; Mismatches 2; Indels 1; Gaps 1;


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; TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
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; FILE REFERENCE:  210121.427CB
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; CURRENT APPLICATION NUMBER:  US/09/352,616A
;
; CURRENT FILING DATE:  1999-07-13
;
; NUMBER OF SEQ ID NOS:  472
;
; SOFTWARE:  FastSeq for Windows Version 3.0
;
; SEQ ID NO 366
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; LENGTH:  1851
;
; TYPE:  DNA
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; ORGANISM:  Homo sapien
;
US-09-352-616A-366

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Query Match	87.9%;	Score 819.8;	DB 4;	Length 1851;
Best Local Similarity	99.6%;	Pred. No. 2.5e-234;		
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DB	1081	CAGGGGACGGCAAGAGCAACGTGGGCACCTCTGGAGACCACAAACGACTCTCTCTGTGAA	1022	
QY	159	GACGCTTGGGAGCAAGAGTGCAAGTGTGTCTGTGCCACTGCTTCCCTCTGTCGAGGGGAG	218	
DB	1021	GACGCTTGGGAGCAAGAGTGCAAGTGTGTCTGTGCCACTGCTTCCCTCTGTCGA-GGGGAG	963	
QY	219	CGCGAAGACCAACGTGGGGCGCTTGGGAGACACTACGATGACAGCGCCTTCATGATCCCAG	278	
DB	962	CGCGAAGACCAACGTGGTTCGCTTGGGAGACTACGATGACAGCGCCTTCATGATCCCAG	903	
QY	279	GTACCACTGTCATGGAGAGATCTTGGACAAGCTCCACAGAGTGCCTGTGGGGTAAAGT	338	
DB	902	GTACCACTGTCATGGAGAGATCTTGGACAAGCTCCACAGAGTGCCTGTGGGGTAAAGT	843	
QY	339	CCCCAGAAAGGATCTCATCGTCACTGCTCAGGACACTGATGTGAAACAAGAGGACAGCA	398	
DB	842	CCCCAGAAAGGATCTCATCGTCACTGCTCAGGACACTGATGTGAAACAAGAGGACAGCA	783	
QY	399	AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGAAATTCAGAAAGTAGTAAAACTCGT	458	
DB	782	AAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGAAATTCAGAAAGTAGTAAAACTCGT	723	
QY	459	GCTGGAACAGAGTGTCAACTTAATGTCTTGGACAACAAAAGAGAGACACTCTGACAAA	518	
DB	722	GCTGGAACAGAGTGTCAACTTAATGTCTTGGACAACAAAAGAGAGACACTCTGACAAA	663	
QY	519	GGCGGTACAAATCCAGGAAGATGAATGTGCTTAATGTTGCTGGAACATGGCACTGATCC	578	
DB	662	GGCGGTACAAATCCAGGAAGATGAATGTGCTTAATGTTGCTGGAACATGGCACTGATCC	603	
QY	579	AAATATTCAGATGAGTAGTGGAAATACCACTCTACACTATGCTGTCTCAATGAAGATAA	638	
DB	602	AAATATTCAGATGAGTAGTGGAAATACCACTCTACACTATGCTGTCTCAATGAAGATAA	543	
QY	639	ATTATGTGGCCAAAGCACTGCTTATACGGTGTGATTCGAAATCAAAAACAAGCATGG	698	
DB	542	ATTATGTGGCCAAAGCACTGCTTATACGGTGTGATTCGAAATCAAAAACAAGCATGG	483	
QY	699	CCTCACACCACCTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT	758	
DB	482	CCTCACACCACCTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT	423	
QY	759	CAAGAAAAAGCGAATTTAAATGCGGTGGATAGATGGAAGACTGCTCTCATCTTGC	818	
DB	422	CAAGAAAAAGCGAATTTAAATGCGGTGGATAGATGGAAGAACTGCTCTCATCTTGC	363	
QY	819	TGTATGTTGTGGATCAGCAAGTATAGTTCAGCCCTCTACTTGGACAAAATGTTGATGTATC	878	
DB	362	TGTATGTTGTGGATCAGCAAGTATAGTTCAGCCCTCTACTTGGACAAAATGTTGATGTATC	303	
QY	879	TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTGTTTCTAGTCATCATCATG	933	
DB	302	TTCTCAAGATCTGGAAGACGGCCAGAGAGTAGTGTGTTTCTAGTCATCATCATG	248	

Query Match	87.9%	Score 819.8	DB 4	Length 1951
Best Local Similarity	99.6%	Pred. No. 2.5e-234		
Matches 832	Conservative 0	Mismatches 2	Indels 1	Gaps 1
QY	99	CAGCGGAGCGGCAAGAGCAACGTGGCACTCTTGGAGACCAACAGACTCCTCTGTGAA	158	
Db	1081	CAGCGGAGCGGCAAGAGCAACGTGGCACTCTTGGAGACCAACAGACTCCTCTGTGAA	1022	
QY	159	GAGCCTTGGAGCAAGAGGTGCAAGTGGTCTGCTGCACTGCTTCCCTGCTGCAAGGGGAG	218	
Db	1021	GAGCCTTGGAGCAAGAGGTGCAAGTGGTCTGCTGCACTGCTTCCCTGCTGCA - GGGGAG	963	
QY	219	CGGCAAGACCAAGTGGCGCTTGGGAGACTACGATGACAGCGCTTCATGATCCCGAG	278	
Db	962	CGGCAAGACCAAGTGGTCTGCTTGGGAGACTACGATGACAGCGCTTCATGATCCCGAG	903	
QY	279	GTACCAAGTCCATGGAGAAAGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGT	338	
Db	902	GTACCAAGTCCATGGAGAAAGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGT	843	
QY	339	CCCAGAAAGGATCTCATGCTCATGCTCAGGACACTGATGTGAAACAGAGGACAGCA	398	
Db	842	CCCAGAAAGGATCTCATGCTCATGCTCAGGACACCGATGTGAACAGAGGACAGCA	783	
QY	399	AAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAAATCAGAAGTAGTAAAACTCGT	458	
Db	782	AAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAAATCAGAAGTAGTAAAACTCGT	723	
QY	459	GCTGGACAGACGATGTCAAATTAAATGCTTTGACAAACAAAAGAGGACAGCTCTGACAAA	518	
Db	722	GCTGGACAGACGATGTCAAATTAAATGCTTTGACAAACAAAAGAGGACAGCTCTGACAAA	663	
QY	519	GGCGGTACAATGCCAGGAAGATGAATGTGCGTTAATGCTGCGAAGTGGCACTGATCC	578	
Db	662	GGCGGTACAATGCCAGGAAGATGAATGTGCGTTAATGCTGCGAAGTGGCACTGATCC	603	
QY	579	AAATATTCCAGATGAGTATGGAATACCCTACACTATGCTGTCTACAATGAAGATAA	638	
Db	602	AAATATTCCAGATGAGTATGGAATACCCTACACTATGCTGTCTACAATGAAGATAA	543	
QY	639	ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAACAGCATGG	698	
Db	542	ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAACAGCATGG	483	
QY	699	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAAT	758	
Db	482	CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTTTAAT	423	
QY	759	CAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC	818	
Db	422	CAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC	363	
QY	819	TGATATGTTGGATCAGCAAGTATAGTACAGCCCTCTACTTGGACAAATGTTGATGATC	878	
Db	362	TGATATGTTGGATCAGCAAGTATAGTACAGCCCTCTACTTGGACAAATGTTGATGATC	303	
QY	879	TTCTCAAGATCTGGAAGACGGCCAGAGATGATGCTGTTTCTAGTCAATCATG	933	
Db	302	TTCTCAAGATCTGGAAGACGGCCAGAGATGATGCTGTTTCTAGTCAATCATG	248	

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RESULT 13
US-09-352-616A-366/c
; Sequence 366, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

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	Query Match	87.9%	Score 819.8;	DB 4;	Length 1851;
	Best Local Similarity	99.6%;	Pred. No. 2,5e-234;		
	Matches 83;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;
Qy	99	CAGGGGAGCGGCAAGAGCAACGTGGGCACCTCTGGAGACCACAAAGACATCCCTCTGTGAA	158		
Db	1081	CAGGGGAGCGGCAAGAGCAACGTGGGCACCTCTGGAGACCACAAAGACATCCCTCTGTGAA	1022		
Qy	159	GAGCGTTGGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGTGCAAGGGGGAG	218		
Db	1021	GACGCTTGGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTTCCCTGTGTCGA-GGGGAG	963		
Qy	219	CGGCAAGAGCAACGTGGGGCGCTTGGGGAGNCTACGATGACAGGCGCTTCATGGATCCCG	278		
Db	962	CGGCAAGAGCAACGTGGTTCGCTTGGGGAGACTACGATGACAGGCGCTTCATGGATCCCG	903		
Qy	279	GTACCAAGCTCCATGGAGAGAAGATCTGGACAAGCTTCCAGAGCTGCCTGGTGGGGTAAAGT	338		

Db	902	GTACCACTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGT	843
Qy	339	CCCCAGAAAGGATCTCATCTCATCTCAGGACACTGATGTGAACAGAGGACACAGCA	398
Db	842	CCCCAGAAAGGATCTCATCTCATCTCAGGACACCGATGTGAACAGAGGACACAGCA	783
Qy	399	AAAGAGGACTGCTCTACATCTCTGGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT	458
Db	782	AAAGAGGACTGCTCTACATCTCTGGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT	723
Qy	459	GCTGCACAGACGATCTCAACTTAATGTCTTGCACACAAAGAGGACAGCTCTGACAAA	518
Db	722	GCTGCACAGACGATCTCAACTTAATGTCTTGCACACAAAGAGGACAGCTCTGACAAA	663
Qy	519	GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTCGTGGAACATGSCACTGATCC	578
Db	662	GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTCGTGGAACATGSCACTGATCC	603
Qy	579	AAATATTCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTACAATGAAGATAA	638
Db	602	AAATATTCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTACAATGAAGATAA	543
Qy	639	ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG	698
Db	542	ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG	483
Qy	699	CCTCACACACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT	758
Db	482	CCTCACACACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT	423
Qy	759	CAAGAAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTTC	818
Db	422	CAAGAAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACTTC	363
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC	878
Db	362	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC	303
Qy	879	TTCTCAGATCTGGAAGACGCGCAGAGATGCTCTTTCTAGTCATCATCATG	933
Db	302	TTCTCAGATCTGGAAGACGCGCAGAGATGCTCTTTCTAGTCATCATCATG	248

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Job time : 99 secs

GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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5	831.8	89.2	879	6	AR405589	AR405589 Sequence
6	831.8	89.2	879	6	AR433323	AR433323 Sequence
7	831.8	89.2	879	6	AX141041	AX141041 Sequence
8	831.8	89.2	879	6	AX200901	AX200901 Sequence
9	831.8	89.2	879	6	AX267557	AX267557 Sequence
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45	819.8	87.9	2184	6	AR278475	AR278475 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AR261059
DEFINITION Sequence 531 from patent US 6321716.
ACCESSION AR261059
VERSION AR261059.1 GI:28071822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 531 27-NOV-2001;
FEATURES Location/Qualifiers

linear PAT 29-JAN-2003

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DB 822 TTCTCAAGATCTGAAAGACGGCCAGAGATATGCTGTTTCTAGTCATCATCATG 876

RESULT 3
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LOCUS AR367286 879 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 531 from patent US 6329505.
ACCESSION AR367286
VERSION AR367286.1 GI:34600261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6329505-A 531 11-DEC-2001;
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ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 158
DB 42 CAGGGGAGCGGACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 101
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QY 339 CCCAGAGAGGATCTCATGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 458
DB 342 AAAGAGGAGTCTCATGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 401
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DB 402 GCTGGACAGAGGATCTCAATTAATGCTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAG 461
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QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGATGCTGTTTCTAGTCATCATCATG 933
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RESULT 4
AR400322
LOCUS AR400322 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 531 from patent US 6620922.
ACCESSION AR400322
VERSION AR400322.1 GI:40143587
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepner,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6620922-A 531 16-SEP-2003;
FEATURES Location/Qualifiers
source 1..879
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Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 158
DB 42 CAGGGGAGCGGACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 101
QY 159 GACGCTTGGGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218
DB 102 GACGCTTGGGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 161
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Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGATGCTGTTTCTAGTCATCATG 933
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RESULT 5
AR405589
LOCUS AR405589 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 531 from patent US 6630305.
ACCESSION AR405589
VERSION AR405589.1 GI:40154426
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 879)
XU,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6630305-A 531 07-OCT-2003;
Location/Qualifiers
1..879
/mol_type="genomic DNA"

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Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCACACACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCACACACTCTCTGTGAA 101
Qy 159 GACGCTTGGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 161
Qy 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGCGCTTCATGATCCAG 278
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Db 582 ATTAATGSCCAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
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Db 642 CTTACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAGAAAAAGCCGAATTTAAATGCGCTGGATAGATATGGAAGCACTGCTCTCATCTTGC 818
Db 702 CAGAAAAAGCCGAATTTAAATGCGCTGGATAGATATGGAAGCACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTCTACTTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGGCAGAGAGATGCTGTTTCTAGTCATCATG 876

RESULT 6
AR433323
LOCUS AR433323 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 314 from patent US 6656480.
ACCESSION AR433323
VERSION AR433323.1 GI:40196105
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 879)
Retter,M.W. and Dillon,D.C.
Compositions and methods for the treatment and diagnosis of breast
cancer
Patent: US 6656480-A 314 02-DEC-2003;
Location/Qualifiers
1..879
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCACACACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCACACACTCTCTGTGAA 101
Qy 159 GACGCTTGGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGGAGCAAGAGTGCATGCTGCTGCTCCCTGCTGAGGGGAG 161
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QY 579 AAATATCCAGATGATGGAATATACCACTCTACACTATGCTGTCTACAATGAAGATAA 638
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QY 819 TGATGTTGTGATCAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 878
Db 762 TGATGTTGTGATCAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 821
QY 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 7
LOCUS AX141041 879 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 531 from Patent WO0134802.
ACCESSION AX141041
VERSION AX141041.1 GI:14281098

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

REFERENCE
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Reed, S. G., Kalos, M. D., Retter, M. W., Stolk, J. A., Day, C. H.,
Skeiky, Y. A., and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0134802-A 531 17-MAY-2001;
CORIXA CORPORATION (US)

FEATURES
Location/Qualifiers
1..879

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ORIGIN

Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGGCGCGCAGAGCAACGCTGGGCACTTCTGGAGACCAACAGACTCTCTCTGTGAA 158
Db 42 CAGGGGGAGCGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGACTCTCTCTGTGAA 101
QY 159 GACGCTTGGGAGCAAGAGGTCGCAAGTGGTGTCTGCCACTCTCTTCCCTGTGAGGGGAG 218
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Db 342 AAGAGGAGCTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 401
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RESULT 8

AX200901

LOCUS AX200901 879 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 531 from Patent WO0151633.
ACCESSION AX200901

VERSION AX200901.1 GI:15390769

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS
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JOURNAL
FEATURES
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Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
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LOCUS
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Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
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Db 702 CAAGAAAAAGCGAAATTTAAATGCGTGTGATATGGAAGCAAGCAAGCAAGCAAG 761
QY 819 TGTATGTTGGATCAGCAAGTATGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAAGCGCGCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933

822 TTCTCAAGATCTGGAAAGCGCGCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876
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ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 158
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Db 402 GCTGGAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTCATGCCAG 461
QY 519 GCGCGTACAAATGCGGAGAGTGAATGCGTAAATGCGTAAATGCGTAAATGCGTAAAT 638
Db 582 ATTAATGGCCAAAGCACTGCTTATACCGTGTGATATCGAATCAAAAGCAAGCATGG 698
QY 582 ATTAATGGCCAAAGCACTGCTTATACCGTGTGATATCGAATCAAAAGCAAGCATGG 641
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QY 759 CAAGAAAAAGCGAAATTTAAATGCGTGTGATATGGAAGCAAGCAAGCAAGCAAGCA 818
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QY 819 TGTATGTTGGATCAGCAAGTATGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGGATCAGCAAGTATGTCAGCCCTCTACTTGGAGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAAGCGCGCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933

Db 582 ATTAATGCCAAAGCACTGCTCTTATACGGTGTCTGATATCGAATCAAAAACAAGCATGG 641
Qy 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT 701
Qy 759 CAAGAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTTACTTGGCAAAAATGTTGATGTATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTTACTTGGCAAAAATGTTGATGTATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
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RESULT 10
AX316977
LOCUS AX316977 879 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 314 from Patent WO0190152.
ACCESSION AX316977
VERSION AX316977.1 GI:17900048
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C., Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
JOURNAL Compositions and methods for the therapy and diagnosis of breast cancer
PATENT: WO 0190152-A 314 29-NOV-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1..879
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTCTGGAGACCACACGACTCTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTCTGGAGACCACACGACTCTCTCTGTGAA 101
Qy 159 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCGCACTTCCCTGCTGCGAGGGGAG 218
Db 102 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCGCACTTCCCTGCTGCGAGGGGAG 161
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTATGGATCCCAG 278
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Qy 279 GTACCAAGTCCATGGAGAAAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGGTAAAGT 338
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Qy 459 GCTGGACAGACGATGTCAACTTAAATGCTTGTGACAAACAAAAGAGGACAGCTCTGACAA 518

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Db 462 GGCCTGACAAATCCAGGAAGATGAATGTCGCTTAAATGTTGCTGGAACATGGCACTGATCC 521
Qy 579 AAATATTCAGATGAGTATGGAATACCACTTACACTTACACTTGTCTCAATGAAGATAA 638
Db 522 AAATATTCAGATGAGTATGGAATACCACTTACACTTGTCTCAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATAGCGTCTGATATCGAATCAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATAGCGTCTGATATCGAATCAAAAACAAGCATGG 641
Qy 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701
Qy 759 CAAGAAAAGCGAATTTAAATGCGCTCGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAGCGAATTTAAATGCGCTCGATAGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATAGTACGCCCTTACTTGGCAAAAATGTTGATGTATC 878
Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCCCTTACTTGGCAAAAATGTTGATGTATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 11
AR261058
LOCUS AR261058 1852 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 530 from patent US 6321716.
ACCESSION AR261058
VERSION AR261058.1 GI:28071821
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Mashiki,Z. and Harada,J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 530 27-NOV-2001;
FEATURES Location/Qualifiers
1..1852
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTCTGGAGACCACACGACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTCTGGAGACCACACGACTCTCTGTGAA 830
Qy 159 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCGCACTTCCCTGCTGCGAGGGGAG 218
Db 831 GACGCTTGGAGCAAGAGGTGCAAGTGGTCTGCGCACTTCCCTGCTGCGAGGGGAG 890
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTATGGATCCCAG 278
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Qy 279 GTACCAAGTCCATGGAGAAAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGGTAAAGT 338
Db 951 GTACCAAGTCCATGGAGAAAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGGTAAAGT 1010
Qy 339 CCCAGAAAGGATCTCATCTGCTGCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA 398

Db 1011 CCCCAGAAAGGATCTCATCGTCATGCTCAGGACACCGGATGTAACAGAGGGCAAGCA 1070
QY 399 AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 458
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QY 459 GGTGACAGACGATGTAACCTTAATGTCCTTGAACAAACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GGTGACAGACGATGTAACCTTAATGTCCTTGAACAAACAAAAGAGGACAGCTCTGACAAA 1190
QY 519 GGCCTGACAAATCCAGGAAGATGAATGTCGTTAATGTTGCTGGAAACATGCACTGATCC 578
Db 1191 GGCCTGACAAATCCAGGAAGATGAATGTCGTTAATGTTGCTGGNAACATGCACTGATCC 1250
QY 579 AAATATTCAGATAGTAGTAAATACCACTTACACTATGCTGTCTCAATAGAGATAA 638
Db 1251 AAATATTCAGATAGTAGTAAATACCACTTACACTATGCTGTCTCAATAGAGATAA 1310
QY 639 ATTAATGTCCTGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAAGCATGG 698
Db 1311 ATTAATGTCCTGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAAAGCATGG 1370
QY 699 CTTACACCACTGCTTACTGTTGATATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAT 758
Db 1371 CTTACACCACTGCTTACTGTTGATATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAT 1430
QY 759 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGACTGCTCTCATCTGTC 818
Db 1431 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGACTGCTCTCATCTGTC 1490
QY 819 TGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAAATGTTGATATC 878
Db 1491 TGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAAATGTTGATATC 1550
QY 879 TTCTCAAGATCTGGAAGACGCGCCAGAGATGCTGTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGACGCGCCAGAGATGCTGTTCTAGTCATCATG 1605

RESULT 12
AR278589
LOCUS AR278589 1852 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 530 from patent US 6512094.
ACCESSION AR278589
VERSION AR278589.1 GI:29712835
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 530 28-JAN-2003;
FEATURES Location/Qualifiers
source 1. .1852
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGACGAGCAAGTGGGCACTCTGAGACCAACAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGCGGCAAGACGAGCAAGTGGGCACTCTGAGACCAACAGCACTCTCTGTGAA 830
QY 159 GAGCGTTGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTGCTTCCCTCTGTCGAGGGGAG 218

Db 831 GAGCGTTGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTCTTCCCTGCTGTCAGGGGAG 890
QY 219 CGGCAAGACCAAGCTGGGCGCTTGGGGAGACTACAGATGACAGCGCTTTCATGGATCCAG 278
Db 891 CGGCAAGACCAAGCTGGTGTGCTTGGGGAGACTACAGATGACAGCGCTTTCATGGATCCAG 950
QY 279 GTACCAAGTCCATGGAGAGATCTGGAACAGCTTCCACAGAGCTGCTGCTGGGTAAAGT 338
Db 951 GTACCAAGTCCATGGAGAGATCTGGAACAGCTTCCACAGAGCTGCTGCTGGGTAAAGT 1010
QY 339 CCCAGAAAGGATCTCATGCTCATGCTCAGGACACTGATGTGAAACAAGAGGGACAAGCA 398
Db 1011 CCCAGAAAGGATCTCATGCTCATGCTCAGGACACTGATGTGAAACAAGAGGGACAAGCA 1070
QY 399 AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 458
Db 1071 AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 1130
QY 459 GCTGGACAGACGATGTAACCTTAATGTCCTTGAACAAACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGGACAGACGATGTAACCTTAATGTCCTTGAACAAACAAAAGAGGACAGCTCTGACAAA 1190
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QY 579 AAATATTCAGATAGTAGTAAATACCACTTACACTATGCTGTCTCAATAGAGATAA 638
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Db 1371 CTTACACCACTGCTTACTGTTGATATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAT 1430
QY 759 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGACTGCTCTCATCTGTC 818
Db 1431 CAGAAAAAAGCGAATTTAAATGCGCTGGATAGATGGAAGACTGCTCTCATCTGTC 1490
QY 819 TGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAAATGTTGATATC 878
Db 1491 TGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGAGCAAAAATGTTGATATC 1550
QY 879 TTCTCAAGATCTGGAAGACGCGCCAGAGATGCTGTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGACGCGCCAGAGATGCTGTTCTAGTCATCATG 1605

RESULT 13
AR367285
LOCUS AR367285 1852 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 530 from patent US 6329505.
ACCESSION AR367285
VERSION AR367285.1 GI:34600260
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Yuqiu, J., Reed, S.G., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A. and Day, C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6329505-A 530 11-DEC-2001;
FEATURES Location/Qualifiers
source 1. .1852
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REFERENCE									
AUTHORS									
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,J.A., Stolk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Sheiky,Y.A.W., Hepler,W.T. and Henderson,R.A.									
TITLE									
Compositions and methods for the therapy and diagnosis of prostate cancer									
JOURNAL									
Patent: US 6620922-A 530 16-SEP-2003;									
Location/Qualifiers									
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/mol_type="genomic DNA"									
ORIGIN									
Query Match 89.2%; Score 831.8; DB 6; Length 1852;									
Best Local Similarity 99.8%; Pred. No. 7.4e-196;									
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	99	CAGGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCACTCTGTGAA	158						
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QY	159	GACGCTTGGGAGCAAGAGTGCAGTGGTGCCTTCCCTGCTGCGAGGGGAG	218						
DB	831	GACGCTTGGGAGCAAGAGTGCAGTGGTGCCTTCCCTGCTGCGAGGGGAG	890						
QY	219	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	278						
DB	891	CGGCAAGAGCAACGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	950						
QY	279	GTACCACTTCATGTCAGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	338						
DB	951	GTACCACTTCATGTCAGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	1010						
QY	339	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	398						
DB	951	GTACCACTTCATGTCAGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	1010						
QY	399	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	458						
DB	1071	CGGCAAGAGCAACGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	1130						
QY	459	GCTGACAGAGCACTCTGTCAGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	518						
DB	1131	GCTGACAGAGCACTCTGTCAGTGGTGCCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCAG	1190						
QY	519	GCCCGTACAAATGCCAGGAGAGTGAATGTGCGTT							

QY 759 CAAGAAAAAGCGAATTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 1431 CAAGAAAAAGCGAATTAAATGCGTGGATAGATATGGAAGAACTGCTCTCATCTTGC 1490
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGTGACAAAATGTTGATGTATC 878
Db 1491 TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGTGACAAAATGTTGATGTATC 1550
QY 879 TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 1605

Search completed: April 30, 2004, 12:25:17
Job time : 3751 secs

RESULT 15
AR405588
LOCUS AR405588 1852 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 530 from patent US 6630305.
ACCESSION AR405588
VERSION AR405588.1 GI:40154425
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 530 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..1852
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 89.2%; Score 831.8; DB 6; Length 1852;
Best Local Similarity 99.8%; Pred. No. 7.4e-196;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGACTCTCTCTGAA 158
Db 771 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGACTCTCTCTGAA 830
QY 159 GACGCTTTGGAGCAAGAGGTGCAAGTGGTGTCTGCCACTGCTTCCCTGTGCAAGGGGAG 218
Db 831 GACGCTTTGGAGCAAGAGGTGCAAGTGGTGTCTGCCACTGCTTCCCTGTGCAAGGGGAG 890
QY 219 CGGCAAGAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCCAG 278
Db 891 CGGCAAGAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCCAG 950
QY 279 GTACACAGTCCATGGAGAAGATCTGGAAGCTCCACAGAGCTGCCCTGGTGGGTAAAGT 338
Db 951 GTACACAGTCCATGGAGAAGATCTGGAAGCTCCACAGAGCTGCCCTGGTGGGTAAAGT 1010
QY 339 CCCAGAAAGGATCTATCGTCATGCTCAGGACACTGTGTGACAGAGGACCAAGCA 398
Db 1011 CCCAGAAAGGATCTATCGTCATGCTCAGGACACTGTGTGACAGAGGACCAAGCA 1070
QY 399 AAGAGGACTGCTCTACATCTGGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT 458
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QY 459 GCTGGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGGACAGCTCTGACAAA 518
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QY 519 GCGCTACAATGCCAGAGAGATGATGCGTTAATGTTGCTGGAAATGCGACTGATCC 578
Db 1191 GCGCTACAATGCCAGAGAGATGATGCGTTAATGTTGCTGGAAATGCGACTGATCC 1250
QY 579 AAATATTCCAGATGAGTATGAAATACCACTCTACACTATGCTCTCTACATGAAGATAA 638
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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: _geneseq2000s.*
4: _geneseq2001as.*
5: _geneseq2001bs.*
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7: _geneseq2003as.*
8: _geneseq2003bs.*
9: _geneseq2003cs.*
10: _geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	913.8	97.9	939	9	Adc15396 Human bre
3	864.2	92.6	1689	8	Abt43733 Molecule
4	835	89.5	876	9	Adc15394 Human bre
5	831.8	88.2	876	9	Adc15393 Human bre
6	831.8	88.2	879	3	Adc81016 Human bre
7	831.8	88.2	879	4	Aah93826 Human pro
8	831.8	88.2	879	4	Aas63919 Human pro
9	831.8	88.2	879	4	Aah85140 Human pro
10	831.8	88.2	879	5	ACA59727 Prostate
11	831.8	88.2	879	6	ABL95290 Human B30
12	831.8	88.2	879	6	Aas98862 Breast tu
13	831.8	88.2	879	7	Adc95454 Prostate
14	831.8	88.2	879	7	Adc1393 Human bre
15	831.8	88.2	879	9	Adc15366 Human bre
16	831.8	88.2	879	9	Adc13981 Human pro
17	831.8	88.2	1852	3	Aac81015 Human pro
18	831.8	88.2	1852	4	Aah93825 Human pro
19	831.8	88.2	1852	4	Aai67210 B305D iso
20	831.8	88.2	1852	4	Aas63918 Human pro
21	831.8	88.2	1852	4	Aah85139 Human pro
22	831.8	88.2	1852	5	ACA59726 Prostate
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ALIGNMENTS

RESULT 1

ADCL5395	ADCL5395 standard; DNA; 933 BP.
ID	ADCL5395
XX	AC
XX	ADCL5395;
DT	18-DEC-2003 (first entry)
XX	Human breast tumour protein DNA, SEQ ID 343.
DE	Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.
XX	Homo sapiens.
XX	WO2003013431-A2.
XX	20-FEB-2003.
PD	05-AUG-2002; 2002WO-US024917.
XX	07-AUG-2001; 2001US-00924400.
PR	20-FEB-2002; 2002US-00079137.
PR	02-AUG-2002; 2002US-00212679.
XX	(CORI-) CORIXA CORP.
XX	Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH; Kalos MD;
XX	WPI; 2003-342398/32.
XX	New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.
PT	Claim 1; SEQ ID NO 343; 308pp; English.
PS	The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells

Aas99861 Breast tu
Acc95453 Prostate
Adc1392 Human bre
Adc15365 Human pro
Adc13980 Human bre
Aav68992 DNA molec
Aav68993 DNA molec
Aaa06531 Human imm
Aac81004 Human B11
Aac81003 Human bre
Aah93707 Human pro
Aai67209 B305D iso
Aas63800 Human pro
Aah02772 Prostate
Aah85021 Human pro
Aca99608 Prostate
Abi95171 Human B30
Aas99849 Breast tu
Aas99849 Breast tu
Abk46893 Human bre
Abk46894 Human bre
ACC95335 Prostate

CC specific for the tumour protein. The present sequence was used to
XX illustrate the invention.

SQ Sequence 933 BP; 272 A; 201 C; 248 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 933; DB 9; Length 933;
Best Local Similarity 100.0%; Pred. No. 6.3e-269;
Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGCGCAAGTGGTCTCTCTCTGTGAGAGGAGCGGCAAGAGCAAC 120
DB 61 AGGAGCAAGATGGCGCAAGTGGTCTCTCTCTGTGAGAGGAGCGGCAAGAGCAAC 120
QY 121 GTGGGCACTTCTGGAGACACACAGACTCTCTGTGAAGAGCGTGGGAGCAAGAGTGC 180
DB 121 GTGGGCACTTCTGGAGACACACAGACTCTCTGTGAAGAGCGTGGGAGCAAGAGTGC 180
QY 181 AAGTGGTGTCTGCACTGCTTCCCTCTCTGAGGGGAGCGGCAAGAGCAAGTGGCGCT 240
DB 181 AAGTGGTGTCTGCACTGCTTCCCTCTCTGAGGGGAGCGGCAAGAGCAAGTGGCGCT 240
QY 241 TGGGAGACTACGATGACAGCGCTTTCATGGATCCAGGTACCAAGTCCATGAGAGAT 300
DB 241 TGGGAGACTACGATGACAGCGCTTTCATGGATCCAGGTACCAAGTCCATGAGAGAT 300
QY 301 CTGAGCAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATCTC 360
DB 301 CTGAGCAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATCTC 360
QY 361 ATGCTCAGGACACTGATGTGAACAAGAGGCAAGCAAGCAAGAGGACTGCTCTACATCTG 420
DB 361 ATGCTCAGGACACTGATGTGAACAAGAGGCAAGCAAGCAAGAGGACTGCTCTACATCTG 420
QY 421 GCCTCTGCCAATGGAATTCAGAGAGTAAAGTCTGCTGTCGACAGAGATGCACTT 480
DB 421 GCCTCTGCCAATGGAATTCAGAGAGTAAAGTCTGCTGTCGACAGAGATGCACTT 480
QY 481 AATGTCTCTGACAAACAAAGAGGACAGCTCTGACAAAGCGGTACAAATGCCAGGAAGAT 540
DB 481 AATGTCTCTGACAAACAAAGAGGACAGCTCTGACAAAGCGGTACAAATGCCAGGAAGAT 540
QY 541 GAATGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGGA 600
DB 541 GAATGTGCGTTAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGGA 600
QY 601 AATACCACTCTACATGCTGCTCAATGAAGATAAATTAATGCCAAAGCACTGCTC 660
DB 601 AATACCACTCTACATGCTGCTCAATGAAGATAAATTAATGCCAAAGCACTGCTC 660
QY 661 TTATAGCGTCTGATATGGAATCAAAAACAGATGCGCTCACACCACTGCTATTGTT 720
DB 661 TTATAGCGTCTGATATGGAATCAAAAACAGATGCGCTCACACCACTGCTATTGTT 720
QY 721 ATACATGAGCAAAAACAGATGCGTGAATTTTAAATCAAGAAAACAGCAATTAAT 780
DB 721 ATACATGAGCAAAAACAGATGCGTGAATTTTAAATCAAGAAAACAGCAATTAAT 780
QY 781 CGCTGGATAGATATGGAAGAACTGCTCTACACTTGTGTGATGTTGGATCAGCAAGT 840
DB 781 CGCTGGATAGATATGGAAGAACTGCTCTACACTTGTGTGATGTTGGATCAGCAAGT 840
QY 841 ATAGTCAGCCCTCTACTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGAGCG 900
DB 841 ATAGTCAGCCCTCTACTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAAGAGCG 900
QY 901 CCAGAGATGATGCTGTTTCTAGTCATCATCATG 933
DB 901 CCAGAGATGATGCTGTTTCTAGTCATCATCATG 933
```

RESULT 2

ADC15396
ID ADC15396 standard; DNA; 939 BP.

XX AC ADC15396;
XX AC ADC15396;
DT 18-DEC-2003 (first entry)

XX Human breast tumour protein DNA, SEQ ID 344.

DE Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
XX ds.

XX Homo sapiens.

XX WO2003013431-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024917.

XX 07-AUG-2001; 2001US-00924400.

XX 20-FEB-2002; 2002US-00079137.

XX 02-AUG-2002; 2002US-00212679.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
XX Kaios MD;

XX WPI; 2003-342398/32.

XX New polynucleotide, useful for preparing a composition for diagnosing,
XX treating or preventing cancer.

XX Claim 1; SEQ ID NO 344; 308pp; English.

XX The present invention relates to compositions and methods for the therapy
XX and diagnosis of cancer, particularly breast cancer. The method for
XX detecting the presence of a cancer in a patient comprises: obtaining a
XX biological sample from the patient; contacting the biological sample with
XX a binding agent that binds to the polypeptide; detecting in the sample an
XX amount of the polypeptide that binds to the binding agent; and comparing
XX the amount of the polypeptide to a predetermined cut-off value. Treating
XX breast cancer comprises administering a composition comprising breast
XX tumour proteins and nucleic acids, which simulates and/or expands T cells
XX specific for the tumour protein. The present sequence was used to
XX illustrate the invention.

SQ Sequence 939 BP; 273 A; 204 C; 249 G; 213 T; 0 U; 0 Other;

Query Match 97.9%; Score 913.8; DB 9; Length 939;

Best Local Similarity 99.1%; Pred. No. 3.6e-263;

Matches 931; Conservative 0; Mismatches 2; Indels 6; Gaps 1;

```
QY 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGCGGCTGCTCTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGCGCAAGTGGTCTCTCTGTGAGAGGAGCGGCAAG 114
DB 61 AGGAGCAAGATGGCGCAAGTGGTCTCTCTGTGAGAGGAGCGGCAAG 120
QY 115 AGCAACCTGGGCACTTCTGGAGACCAACAGACTCTCTGTGAAGAGCGTGGAGCAAG 174
DB 121 AGCAACCTGGGCACTTCTGGAGACCAACAGACTCTCTGTGAGAGCGTGGAGCAAG 180
QY 175 AGGTGCAAGTGGTCTGCTGCACTGCTTCCCTGTGAGGGGAGCGCAAGCAAGT 234
DB 181 AGGTGCAAGTGGTCTGCTGCACTGCTTCCCTGTGAGGGGAGCGCAAGCAAGT 240
QY 235 GGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAGGTACCACTCCATGGA 294
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PR	13-JUL-2001; 2001US-0305324P.
PR	19-JUL-2001; 2001US-0307003P.
PR	27-JUL-2001; 2001US-0308185P.
PR	03-AUG-2001; 2001US-0310096P.
PR	10-AUG-2001; 2001US-0311511P.
PR	08-MAR-2002; 2002US-0363619P.
XX	(INCY-) INCYTE GENOMICS INC.
EA	Thornton M, Au-Young JK, Azimzai Y, Bandman O, Barroso I;
XX	Baughn MR, Becha SD, Borowsky ML, Ding L, Duggan BM, Elliott VS;
PI	Emerling BM, Forsythe BJ, Gandhi AR, Gietzen KJ, Gorvaid AE;
PI	Griffin JA, Gururajan R, Hafalia AJA, Ring HZ, Jeon CH, Jones KA;
PI	Lal PG, Lee EA, Lee S, Li JX, Lu DAM, Marquis JP, Lehr-Mason PM;
PI	Chawla NK, Arvizu CS, Sanjanwalia B, Sorriasse T, Swarnakar A;
PI	Tang YT, Thangavelu K, Tran B, Tran UK, Warren BA, Xu Y, Yao MG;
PI	Yang H, Yue H, Zebardjian Y, Chang H;
XX	WPI; 2003-533003/50.
DR	P-PSDB; ABJ39131.
DR	
XX	New Molecules for Disease Detection and Treatment polypeptides, useful
PT	for preparing a composition for diagnosing or treating e.g.
PT	cardiovascular or neurological disorders.
XX	
XX	Claim 5; Page 276; 289pp; English.
CC	This invention relates to novel polypeptides associated with Molecules
CC	for Disease Detection and Treatment (MDT) and the cDNA sequences which
CC	encode them. MDT-antagonists, MDT-agonists or gene therapy may produce
CC	cardiant, cytostatic and neuroprotective activities. The polypeptides and
CC	cDNA sequences of the invention may be useful for the preparation of a
CC	composition for the diagnosis or treatment of a disease which is
CC	associated with decreased expression or over-expression of functional
CC	MDT proteins, for example cardiovascular, neurological, cell
CC	proliferative, autoimmune/inflammatory or developmental disorders. They
CC	may also be useful in the treatment and diagnosis of cancer, diseases
CC	treated with steroids and disorders caused by the metabolic response to
CC	treatment with steroids. The present sequence is the cDNA sequence
CC	encoding a human Molecule for Disease Detection and Treatment (MDT) of
CC	the invention
XX	
SQ	Sequence 1689 BP; 499 A; 360 C; 431 G; 399 T; 0 U; 0 Other;
XX	
Query Match	92.6%; Score 864.2; DB 8; Length 1689;
Best Local Similarity	98.6%; Pred. No. 3, 8e-248;

Qy	1	ATGGTGGTTGAGGTTGATTCAATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTGGTCTC	60
Db	28	ATGGTGGCTGAGGTTGATTCAATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTGGTCTC	87
Qy	61	AGGAGCAGATATGGCAAGTGGTG-----CTGCTTTCCTGCTCTGCAGGGGGAGCGGCAAG	114
Db	88	AGGAGCAAGATGGCAAGTGGTGCTGTCACCTGCTTTCCTGCTCTGCAGGGGGAGCGGCAAG	147
Qy	115	AGCAACTGTGGGCACTCTTCGAGAGCCACAAACGACTCCTCTGTGAAGACGCTTTGGGAGCAAG	174
Db	148	AGCAACTGTGGGCACTCTTCGAGAGCCACAAACGACTCCTCTGTGAAGACGCTTTGGGAGCAAG	207
Qy	175	AGGTGCAAGTGTGTGCTGCCACTGTTCCCTCTGTCAGGGGGAGCGGCAAGAGCAACGTG	234
Db	208	AGGTGCAAGTGTGTGCTGCCACTGTTCCCTCTGTCAGGGGGAGCGGCAAGAGCAACGTG	267
Qy	235	GGCGCTTTGGGAGACTACGATGACAGCGCTTTCATGGATCCAGGTTACCAAGTCCATGGA	294
Db	268	GTGCGTTGGGAGACTACGATGACAGCGCGCTTCATGGATCCAGGTTACCAAGTCCATGGA	327
Qy	295	GAGATCTGGACAAGCTCCACAGAGTGCCTGTGGGTAAAGTCCCCAGAAAGGATCTC	354
Db	328	GAGATCTGGACAAGCTCCACAGAGTGCCTGTGGGTAAAGTCCCCAGAAAGGATCTC	387
Qy	355	ATCGTCAATGCTCAGGAGCACTGATGTGAACAAGAGGGACCAAGCAAAAGAGGACTGCTCTA	414

Db 388 ATCGTCATGCTCAGGACACGATGTGAACAAGGACAGGCAAGCAAAAGAGAGACTGCTCTA 447
Qy 415 CATCTGGCTCTGCCAATGGGAATCAGAAAGTAGTAAACTGCTGCTGGACAGACGATGT 474
Db 448 CATCTGGCTCTGCCAATGGGAATCAGAAAGTAGTAAACTGCTGCTGGACAGACGATGT 507
Qy 475 CAACTTAATGCTCTTGACAAACAAAAGAGACAGCTCTTGACAAAGCCGCTCAATGCCAG 534
Db 508 CAACTTAATGCTCTTGACAAACAAAAGAGACAGCTCTTGACAAAGCCGCTCAATGCCAG 567
Qy 535 GAAGATGAATGCGTGAATGCTGGAACATGCACTGATGCACTGATGCACTGATGCACTGATG 594
Db 568 GAAGATGAATGCGTGAATGCTGGAACATGCACTGATGCACTGATGCACTGATGCACTGATG 627
Qy 595 TATGAAATACCACTCTACACTATGCTGTCTACATGAAGATAAATTAATGSCCAAGCA 654
Db 628 TATGAAATACCACTCTACACTATGCTGTCTACATGAAGATAAATTAATGSCCAAGCA 686
Qy 655 CTGCTCTTATACGCTCTGATATCGAATCAAAACCAAGCATGGCTCACACCTGCTA 714
Db 687 CTGCTCTTATACGCTCTGATATCGAATCAAAACCAAGCATGGCTCACACCTGCTA 745
Qy 715 CTGCTCTTATACGCTCTGATATCGAATCAAAACCAAGCATGGCTCACACCTGCTA 774
Db 746 CTGCTCTTATACGCTCTGATATCGAATCAAAACCAAGCATGGCTCACACCTGCTA 803
Qy 775 TTAATGCGCTGATATGGAAGAACTGCTCTCATATCTGCTGATGTTGATGATCA 834
Db 804 TTAATGCGCTGATATGGAAGAACTGCTCTCATATCTGCTGATGTTGATGATCA 863
Qy 835 GCAAGTATAGTACGCTCTTACTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAA 894
Db 864 GCAAGTATAGTACGCTCTTACTGAGCAAAATGTTGATGATCTTCTCAAGATCTGGAA 923
Qy 895 AGACGCGCAGAGATGATGCTGTTCTTCTAGTCATCATG 933
Db 924 AGACGCGCAGAGATGATGCTGTTCTTCTAGTCATCATG 962

RESULT 4
ADCL5394
ID ADC15394 standard; DNA; 876 BP.
XX
AC ADCL5394;
XX
DT 18-DEC-2003 (first entry)
DE Human breast tumour protein DNA, SEQ ID 342.
XX
KW Cystostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW ds.
XX Homo sapiens.
OS
FN WO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR WP1; 2003-342398/32.
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,

PT treating or preventing cancer.
XX Claim 1; SEQ ID NO 342; 308pp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;
Query Match 89.5%; Score 835; DB 9; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.5e-239;
Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 101
Qy 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGGAGCAAGAGGTGCAAGTGGTCTGCCACTGCTCCCTGCTGAGGGGAG 161
Qy 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTAGATGACAGCGCCCTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTAGATGACAGCGCCCTTCATGATCCAG 221
Qy 279 GTACACGCTCCATGGAGAAGATCTGGACAGCTCCACAGAGCTGCTGTTGGGTTAAGT 338
Db 222 GTACACGCTCCATGGAGAAGATCTGGACAGCTCCACAGAGCTGCTGTTGGGTTAAGT 281
Qy 339 CCCAGAGAAAGATCTCATCTGCTCATGCTCAGGACACTGATGTAACAGAGGGAACAAGCA 398
Db 282 CCCAGAGAAAGATCTCATCTGCTCATGCTCAGGACACTGATGTAACAGAGGGAACAAGCA 341
Qy 399 AAAGAGACTGCTCTACATCTGGCTCTGCCATGGGAATTCAGAACTGTAACCTCGT 458
Db 342 AAAGAGACTGCTCTACATCTGGCTCTGCCATGGGAATTCAGAACTGTAACCTCGT 401
Qy 459 GCTGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGGACAGCTCTGACAAA 461
Qy 519 GGGCGTCAATGCGCAGGAAGATGATGCTGTTAATGTTGCTGGAACATGCGACTGATCC 578
Db 462 GGGCGTCAATGCGCAGGAAGATGATGCTGTTAATGTTGCTGGAACATGCGACTGATCC 521
Qy 579 AAATATCCAGATGATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 638
Db 522 AAATATCCAGATGATGGAATACCACTCTACACTATGCTCTACATGAAGATAA 581
Qy 639 ATTAATGCCAAAGCACTGCTCTTATAGCGTGTGATATGGAATCAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTCTTATAGCGTGTGATATGGAATCAAAAACAGCATGG 641
Qy 699 COTCAACCACTGCTCTTATAGCGTGTGATATGGAATCAAAAACAGCATGG 758
Db 642 COTCAACCACTGCTCTTATAGCGTGTGATATGGAATCAAAAACAGCATGG 701
Qy 759 CAAGAAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGTGATCAGCAAGTATAGTACGCTCTTACTTGTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGATCAGCAAGTATAGTACGCTCTTACTTGTGAGCAAAATGTTGATGATC 821

QY 879 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
DB 822 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 5

ADCL5393
ID ID ADC15393 standard; DNA; 876 BP.

AC AC ADC15393;

DT 18-DEC-2003 (first entry)

XX Human breast tumour protein DNA, SEQ ID 341.

XX Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
ds.

XX Homo sapiens.

OS WO2003013431-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024917.

XX 07-AUG-2001; 2001US-00924400.

PR 20-FEB-2002; 2002US-00079137.

PR 02-AUG-2002; 2002US-00212679.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;

PI Kalos MD;

XX WPI; 2003-342398/32.

XX New polynucleotide, useful for preparing a composition for diagnosing,

XX treating or preventing cancer.

XX Claim 1; SEQ ID NO 341; 308pp; English.

XX The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.

XX SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;

Query Match 89.2%; Score 831.8; DB 9; Length 876;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACGTTGGGCACTTCTGGAGACCAACGACTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAACGTTGGGCACTTCTGGAGACCAACGACTCTCTGTGAA 101

QY 159 GACGCTTGGGAGCAGAGGTCAAGTGTGCTGCCACTGCTTCCCTGCTGCAGGGGGAG 218
DB 102 GACGCTTGGGAGCAGAGGTCAAGTGTGCTGCCACTGCTTCCCTGCTGCAGGGGGAG 161

QY 219 CGGCAAGAGCAACGTTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 278
DB 162 CGGCAAGAGCAACGTTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 221

QY 279 GTACACGCTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGGGTAAAGT 338
DB 222 GTACACGCTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGGGTAAAGT 281
QY 339 CCCAGAAAAGGATCTCATCGTCTCAGGCACTGATGTAACAAGAGGGACAAGCA 398
DB 282 CCCAGAAAAGGATCTCATCGTCTCAGGCACTGATGTAACAAGAGGGACAAGCA 341
QY 399 AAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTG 458
DB 342 AAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTG 401
QY 459 GCTGGACAGACGATGTCAACTTAATGCTTGAACAACAAAAGAGGACAGCTCTGACAAA 518
DB 402 GCTGGACAGACGATGTCAACTTAATGCTTGAACAACAAGAGGACAGCTCTGACAAA 461
QY 519 GGCCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTGTGGCAACATGGCACTGATCC 578
DB 462 GGCCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTGTGGCAACATGGCACTGATCC 521
QY 579 AAATATTCAGATGATGGAATACCACTACACTATCTGTCTACAATGAAGATAA 638
DB 522 AAATATTCAGATGATGGAATACCACTACACTATCTGTCTACAATGAAGATAA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGTTGCTGATATCGAATCAAAAACAAGCATGG 698
DB 582 ATTAATGGCCAAAGCACTGCTCTTATACGTTGCTGATATCGAATCAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGTGTATACATGACAAAACAGCAAGTGGTGAATTTTAAAT 758
DB 642 COTCACACCACTGCTACTTGTGTATACATGACAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATACTTGC 818
DB 702 CAAGAAAAAAGCGAATTTAAATGCGCTGATATGGAAGAACTGCTCTCATACTTGC 761
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTCAGGCTTCTACTTGGCAAAATGTTGATGATC 878
DB 762 TGTATGTTGTGGATCAGCAAGTATAGTCAGGCTTCTACTTGGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
DB 822 TTCTCAAGATCTGAAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 6

AAC81016
ID AAC81016 standard; cDNA; 879 BP.

XX AAC81016;

XX 13-FEB-2001 (first entry)

DE Human breast tumour-specific antigen cDNA SEQ ID NO: 314.

XX Human; breast tumour-specific antigen; cytostatic; vaccine;

XX breast cancer; B18Ag1; B11Ag1; B15Ag1; B8;

OS Homo sapiens.

PN WO200061753-A2.

XX 19-OCT-2000.

XX 07-APR-2000; 2000WO-US009312.

XX 09-APR-1999; 99US-00289198.

PR 28-OCT-1999; 99US-00429755.

PR 23-MAR-2000; 2000US-00534825.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;

XX MPI: 2000-628403/60.
DR P-PSDB; AAB28636.
XX

PT An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient.
XX

PS Claim 4; Page 185-186; 187pp; English.

XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-Cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX

XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 89.2%; Score 831.8; DB 3; Length 879;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 99 CAGGGGAGCGGCACAGACCAAGCTGGGCACCTCTGGAGACCAACAGCACTCCTCTGTGAA 158
DB |||||
QY 159 GAGCGTTGGAGCAAGAGGTGCAAGTGGTGTGCCACTGTCCCTGTGTGAGGGGGAG 218
DB |||||
QY 162 GACGCTTGGAGCAGAGGTGCAAGTGGTGTGCCACTGTCTCCCTGTGTGAGGGGGAG 161
QY 219 CGGCACAGCAGCGTGGGCGCTTGGGAGACTACGATCAGACGCGCTTCATGATCCCCAG 278
DB |||||
QY 279 GTACCAAGTCCATGGAGAAAGTCTGGCAAGCTCCACAGAGTGCCTGTGGGGTAAAGT 338
DB |||||
QY 339 CCCAGAGAAAGATCTCATCGTATGCTCAGGGACACTGATGTGACAAAGAGGACAGCA 398
DB |||||
QY 341 CCCAGAGAAAGATCTCATCGTATGCTCAGGACACGGATGTGAACAAAGAGGACAGCA 341
QY 399 AAAGAGACTGCTCTACATCTGGCGCTTCGCCAATGGGAATTCAGAAGTAGTAAACTCGT 458
DB |||||
QY 342 AAAGAGACTGCTCTACATCTGGCGCTTCGCCAATGGGAATTCAGAAGTAGTAAACTCGT 401
QY 459 GCTGGACAGACGATGTCAACTTAATGCTCTTGACAAACAAAGAGGACGCTCTGCACAA 518
DB |||||
QY 461 GCTGGACAGACGATGTCAACTTAATGCTCTTGACAAACAAAGAGGACGCTCTGCACAA 461
QY 519 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAAACATGGCACTGATCC 578
DB |||||
QY 462 GGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAAACATGGCACTGATCC 521
QY 579 AAATATTCCAGATGAGTATGGAAATACCACTTACACTATGCTCTCTACATGAAGATAA 638
DB |||||
QY 522 AAATATTCCAGATGAGTATGGAAATACCACTTACACTATGCTCTCTACATGAAGATAA 581
QY 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAACAAAGCATGG 698
DB |||||
QY 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGCTGATATCGAATCAAAAACAAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758
DB |||||
QY 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701

Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GACCTTTGGGAGCAAGAGTGTCAAGTGTCTGCTGCCACTGTTCCCTGCTGACGGGGAG 218
Db 102 GACCTTTGGGAGCAAGAGTGTCAAGTGTCTGCTGCCACTGTTCCCTGCTGACGGGGAG 161
QY 219 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221
QY 279 GTACCCAGTCCATGGAGAGTCTGGCAAGCTCCAGAGCTCCAGAGCTGCTGGTGGGTTAAAGT 338
Db 222 GTACCCAGTCCATGGAGAGTCTGGCAAGCTCCAGAGCTGCTGGTGGGTTAAAGT 281
QY 339 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 398
Db 282 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 341
QY 399 AAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTACTAAACTCGT 458
Db 342 AAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTACTAAACTCGT 401
QY 459 GCTGGACAGAGTGTCAACTTAATGTCTTGTGACCAACAAAGAGGACAGCTCTGCAAA 518
Db 402 GCTGGACAGAGTGTCAACTTAATGTCTTGTGACCAACAAAGAGGACAGCTCTGCAAA 461
QY 519 GGGCGTCAATGCCAGGAAGTGAATGTGGCTTAATGTGCTGGAACATGCGACTGATCC 578
Db 462 GGGCGTCAATGCCAGGAAGTGAATGTGGCTTAATGTGCTGGAACATGCGACTGATCC 521
QY 579 AAATATTCAGATGATGAATATACACTCTACACTATGCTCTACAAATGAAGATAA 638
Db 522 AAATATTCAGATGATGAATATACACTCTACACTATGCTCTACAAATGAAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTTTATAGGTGCTGATATGGAATCAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTTTATAGGTGCTGATATGGAATCAAAACAGCATGG 641
QY 699 CCTCACCCACTGCTACTTGTATACATGACCAAAACAGCACTGCTGGAATTTTAAAT 758
Db 642 CCTCACCCACTGCTACTTGTATACATGACCAAAACAGCACTGCTGGAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 818
Db 702 CAAGAAAAAGCGAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 761
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTACGCTTACTTGGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGGATCAGCAAGTATAGTACGCTTACTTGGCAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 8
AAS63919
ID AAS63919 standard; cdna; 879 BP.
XX
AC AAS63919;
XX
DT 29-JAN-2002 (first entry)
DE Human prostate cdna clone B305D splice variant #11 open reading frame.
XX Human; prostate cancer; ss; cytosatic; immunostimulant; tumour.
XX Homo sapiens.
XX WO200173032-A2.
XX
PD 04-OCT-2001.
XX

PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter WM, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-539232/73.
DR P-PSDB; AAU69821.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 1; Page 408; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
polypeptides, fusion proteins of the polypeptides, antibodies raised
against the polypeptides (or antigenic epitopes derived from them) and
antigen-presenting cells expressing the polypeptides. The antibodies are
useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
useful for stimulating and/or expanding T cells specific for a tumour
protein, and for inhibiting the development of cancer especially prostate
cancer. Compositions comprising the polynucleotide and/or polypeptide are
useful for stimulating an immune response, and for treating cancer. The
oligonucleotide is useful for detecting cancer. The present sequence is a
prostate specific polynucleotide of the invention
XX
XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
Query Match 89.2%; Score 831.8; DB 4; Length 879;
Best Local Similarity 99.8%; Pred. NO. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GACGCTTGGGAGCAAGAGGTGCAAGTGTGCTGCCACTCTTCCCTGCTGAGGGGAG 218
Db 102 GACGCTTGGGAGCAAGAGGTGCAAGTGTGCTGCCACTCTTCCCTGCTGAGGGGAG 161
QY 219 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 278
Db 162 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGATCCAG 221
QY 279 GTACCCAGTCCATGGAGAGTCTGGCAAGCTCCAGAGCTGCTGGTGGGTTAAAGT 338
Db 222 GTACCCAGTCCATGGAGAGTCTGGCAAGCTCCAGAGCTGCTGGTGGGTTAAAGT 281
QY 339 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 398
Db 282 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGACAGCA 341
QY 399 AAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTACTAAACTCGT 458
Db 342 AAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTACTAAACTCGT 401
QY 459 GCTGGACAGAGTGTCAACTTAATGTCTTGTGACCAACAAAGAGGACAGCTCTGCAAA 518


```

ACA59727
ID ACA59727 standard; cDNA; 879 BP.
XX AC
XX ACA59727;
XX XX
DT 10-JUN-2003 (first entry)
XX DE
XX Prostate cancer therapy associated cDNA #464.
XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW pSMA; gene; ss.
XX OS Homo sapiens.
XX US US2002192763-A1.
XX PD 19-DEC-2002.
XX PF 29-JUN-2001; 2001US-00895793.
XX PR 04-OCT-1999; 99US-015745SP.
XX PR 04-OCT-2000; 2000US-00679272.
XX PR 28-MAR-2001; 2001US-00822827.
XX XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEL/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA,
XX McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX WPI; 2001-245062/25.
XX XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX XX
XX Example 11; SEQ ID NO 531; 85pp; English.
XX CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at

```

CC	seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX	
QQ	Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
	Query Match 89.28; Score 831.8; DB 5; Length 879;
	Best Local Similarity 99.88; Pred. No. 1.4e-238; Indels 0; Gaps 0;
	Matches 833; Conservative 0; Mismatches 2;
Qy	99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAAAGACTCCTCTGTGAA 158
Db	42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAAAGACTCCTCTGTGAA 101
Qy	159 GACGCTTGGAGCAAGAGGTGCAAGTGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 218
Db	102 GACGCTTGGAGCAAGAGGTGCAAGTGTCTGCCACTGCTTCCCTGCTGCGAGGGGAG 161
Qy	219 CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCCCTTCATGGATCCAG 278
Db	162 CGGCAAGAGCAACGCTGGTCTTGGGAGACTACGATGACAGCGCCCTTCATGGATCCAG 221
Qy	279 GTACCAAGTCCATGGAGAGATCTGACAAAGCTCCACAGAGCTGCTGTTGGGTAAAGT 338
Db	222 GTACCAAGTCCATGGAGAGATCTGACAAAGCTCCACAGAGCTGCTGTTGGGTAAAGT 281
Qy	339 CCCAGAAAGGATCTCATCTGCTCATGCTCAGGGAACATGATGTGAACAAGAGGGACAAGCA 398
Db	282 CCCAGAAAGGATCTCATCTGCTCATGCTCAGGGAACATGATGTGAACAAGAGGGACAAGCA 341
Qy	399 AAGAGAGCTGCTTCAATCTGGCCCTCTGCCAATGGGAAATCGAAGTAGTAAACCTCGT 458
Db	342 AAGAGAGCTGCTTCAATCTGGCCCTCTGCCAATGGGAAATCGAAGTAGTAAACCTCGT 401
Qy	459 GCTGGACAGACGATGTCAACTTAATGCTTGAACAACAAAAGAGGACAGCTCTGACAA 518
Db	402 GCTGGACAGACGATGTCAACTTAATGCTTGAACAACAAAAGAGGACAGCTCTGACAA 461
Qy	519 GGCCGTACAATGCCAGAGATGAATGTGCGTTTAATGTTGCTGGAACTGGCACTGATCC 578
Db	462 GGCCGTACAATGCCAGAGATGAATGTGCGTTTAATGTTGCTGGAACTGGCACTGATCC 521
Qy	579 AATATTTCCAGATGAGTAGGAAATACCCTCTACACTATGCTGTCTACAAATGAAGATA 638
Db	522 AATATTTCCAGATGAGTAGGAAATACCCTCTACACTATGCTGTCTACAAATGAAGATA 581
Qy	639 ATTAATGGCCAAAGCACTGCTCTTTACGGTGTGTATCGAATCAAAAACCAAGCATGG 698
Db	582 ATTAATGGCCAAAGCACTGCTCTTTACGGTGTGTATCGAATCAAAAACCAAGCATGG 641
Qy	699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAT 758
Db	642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAT 701
Qy	759 CAAGAAAAAGCGAAATTTAAATCGCTGGATAGATGGAAGAACTGCTCTCATACTTGC 818
Db	702 CAAGAAAAAGCGAAATTTAAATCGCTGGATAGATGGAAGAACTGCTCTCATACTTGC 761
Qy	819 TGTATGTTGGATCAGCAAGTAGTAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGTATC 878
Db	762 TGTATGTTGGATCAGCAAGTAGTAGTCAGCCCTCTACTTGGAGCAAAATGTTGATGTATC 821
Qy	879 TTCTCAAGATCTGGAAGACGGCCAGAGACTATGCTGTTTCTAGTCAATCATCATG 933
Db	822 TTCTCAAGATCTGGAAGACGGCCAGAGACTATGCTGTTTCTAGTCAATCATCATG 876
RESULT 11	
ABL95290	
ID	ABL95290 standard; cdna; 879 BP.
XX	
AC	ABL95290;
XX	
DT	19-JUL-2002 (first entry)
XX	

XX Homo sapiens.
 XX WO200190152-A2.
 XX 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-US016776.
 XX 24-MAY-2000; 2000US-00577505.
 XX 08-JUN-2000; 2000US-00590583.
 XX 26-OCT-2000; 2000US-00699295.
 XX 16-MAR-2001; 2001US-00810936.
 XX (CORI-) CORIXA CORP.
 XX Prudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 XX Wang A, Skeiky YAW, Harlocker SL, Day CH;
 XX P-PSDB; AAU74385.
 XX New breast tumor proteins and polynucleotides encoding them, useful for
 XX treating and/or preventing cancer, particularly breast cancer, and for
 XX eliciting humoral and/or cellular immune response.
 XX Claim 1; Page 231-232; 245pp; English.
 XX The invention relates to novel breast tumour polynucleotides and
 XX polypeptides. The polypeptides and polynucleotides are useful in
 XX pharmaceutical compositions for treating and/or preventing cancer,
 XX particularly breast cancer, and for eliciting an immune response,
 XX may be used as probes or primers for nucleic acid hybridisation, in the
 XX design and preparation of ribozyme molecules for inhibiting expression of
 XX tumour polypeptides and proteins, and in recombinant DNA molecules to
 XX direct expression of a polypeptide in host cells. AAS99570-AAS99988
 XX represent novel human breast cancer protein coding sequences and PCR
 XX primers of the invention
 XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
 XX Query Match 89.2%; Score 831.8; DB 6; Length 879;
 XX Best Local Similarity 99.8%; Pred. No. 1.4e-238;
 XX Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCAACAGCACTCTGTGAA 158
 DB 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCAACAGCACTCTGTGAA 101
 QY 159 GACGCTTGGGAGCAAGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
 DB 102 GACGCTTGGGAGCAAGAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
 QY 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGCACTACGATGACAGCGCTTCATGGATCCAG 278
 DB 162 CGGCAAGAGCAACGTGGTGGTGGGAGCACTACGATGACAGCGCTTCATGGATCCAG 221
 QY 279 GTACACGTCATCGGAGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 338
 DB 222 GTACACGTCATCGGAGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 281
 QY 339 CCCGAGAAGGATCTCATGCTCATGCTCAGGCACTGTGTGAACAAGAGGACAGCA 398
 DB 282 CCCGAGAAGGATCTCATGCTCATGCTCAGGCACTGTGTGAACAAGAGGACAGCA 341
 QY 399 AAAGAGGAGTCTCTACATCTGGCTCTGGCAATGGGAATTCAGAGTAGTAAACTCGT 458
 DB 342 AAAGAGGAGTCTCTACATCTGGCTCTGGCAATGGGAATTCAGAGTAGTAAACTCGT 401
 QY 459 GCTGGACAGAGTCTCAACTATATGCTTGTGACCAACAAGAGGACAGCTCTGCAAA 518
 DB 402 GCTGGACAGAGTCTCAACTATATGCTTGTGACCAACAAGAGGACAGCTCTGCAAA 461

QY 519 GGCGCTACAAATGCCAGGAGATGAATGTGGCTTAATTTGCTGGCAACATGGCACTGATCC 578
 DB 462 GGCGGTACAAATGCCAGGAGATGAATGTGGCTTAATTTGCTGGCAACATGGCACTGATCC 521
 QY 579 AAATATTCAGATGAGTATGGAAATACCACTTACATCTACTGCTGTCTCAATGAAGATAA 638
 DB 522 AAATATTCAGATGAGTATGGAAATACCACTTACATCTACTGCTGTCTCAATGAAGATAA 581
 QY 639 ATTAATGGCCAAAGCACCTGCTTATAGGCTGCTGATATCGAATCAAAAAACAAGCATGG 698
 DB 582 ATTAATGGCCAAAGCACCTGCTTATAGGCTGCTGATATCGAATCAAAAAACAAGCATGG 641
 QY 699 CCTCACACCACTGCTACTTGTATACATGACAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
 DB 642 CCTCACACCACTGCTACTTGTATACATGACAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
 QY 759 CAAGAAAAAAGCGAATTTAAATGCCCTGATAGATATGGAAGAACTGCTCTCATACTTGC 818
 DB 702 CAAGAAAAAAGCGAATTTAAATGCCCTGATAGATATGGAAGAACTGCTCTCATACTTGC 761
 QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAAGCCCTCTACTTGGACAAATGTTGATGTATC 878
 DB 762 TGTATGTTGTGATCAGCAAGTATAGTCAAGCCCTCTACTTGGACAAATGTTGATGTATC 821
 QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
 DB 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 13

ACC95454
 ID ACC95454 standard; cDNA; 879 BP.

XX ACC95454;

XX AC

XX 28-AUG-2003 (first entry)

XX Prostate tumour specific cDNA sequence SEQ ID 531.

XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;

XX immune response; prostate cancer; ss.

XX Homo sapiens.

XX WO200289747-A2.

XX 14-NOV-2002.

XX 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

XX 29-JUN-2001; 2001US-00895814.

XX 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;

XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;

XX Carter D, Li SX, Wang A, Skeiky YAW, Hesler WT, Hural J;

XX McNeill PD, Houghton RL, Vinals Y De Bassolc, Foy TM, Matanabe Y;

XX Deng T;

XX WPI; 2003-167130/16.

XX New prostate-specific proteins and genes, useful in gene therapy,

XX particularly for stimulating an immune response in a patient, or treating

XX prostate cancer in a patient, as well as for diagnosing prostate cancer

XX in a patient.

XX Example 11; Page 475; 691pp; English.

XX The present invention relates to novel prostate-specific proteins (PSP)

CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention

XX
SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
Query Match 89.2%; Score 831.8; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GAGCTTTGGAGCAAGAGGTCAGGTCCTCCCTGCTGAGGGGGAG 218
Db 102 GAGCTTTGGAGCAAGAGGTCAGGTCCTCCCTGCTGAGGGGGAG 161
QY 219 CGCAAGAGCAACGCTGGGCGCTTTGGGAGACTACGATGACAGGCTTCCATGATCCAG 278
Db 162 CGCAAGAGCAACGCTGGGCGCTTTGGGAGACTACGATGACAGGCTTCCATGATCCAG 221
QY 279 GTACCAAGCTCCAGAGAGATCTGACAGCTCCAGAGCTGCTGCTGGGTTAACT 338
Db 222 GTACCAAGCTCCAGAGAGATCTGACAGCTCCAGAGCTGCTGCTGGGTTAACT 281
QY 339 CCCAGAAAGGATCTCATCTGCTGCTCAGGACACTGTGTAACAAGAGGACAAAGCA 398
Db 282 CCCAGAAAGGATCTCATCTGCTGCTCAGGACACTGTGTAACAAGAGGACAAAGCA 341
QY 399 AAGAGAGCTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
Db 342 AAGAGAGCTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401
QY 459 GCTGACAGAGCTGCTCACTTAATGCTTGTGCAACAAAGAGGACAGCTCTGACAA 518
Db 402 GCTGACAGAGCTGCTCACTTAATGCTTGTGCAACAAAGAGGACAGCTCTGACAA 461
QY 519 GCGCGTCAATGCCAGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
Db 462 GCGCGTCAATGCCAGAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521
QY 579 AATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
Db 522 AATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 581
QY 639 ATTATGGCCAAAGCACTGCTCTTATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
Db 582 ATTATGGCCAAAGCACTGCTCTTATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
QY 699 CTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
Db 642 CTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
QY 759 CAAGAAAAAGCAATTTAAATGGCTGGATAGATGATGATGATGATGATGATGATGATGATGAT 818
Db 702 CAAGAAAAAGCAATTTAAATGGCTGGATAGATGATGATGATGATGATGATGATGATGATGAT 761
QY 819 TGTATGTTGGATCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
Db 762 TGTATGTTGGATCAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
QY 879 TTCTCAAGATCTGGAAGAGCGGCGAGAGATGATGCTGCTTCTAGTCATCATCATG 933
Db 822 TTCACAGATCTGGAAGAGCGGCGAGAGATGATGCTGCTTCTAGTCATCATCATG 876

RESULT 14
ID ADAL1393
XX ADAL1393 standard; cDNA; 879 BP.

AC ADAL1393;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human breast cancer specific full length cDNA B305D-A ORF.
XX
KW ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002165371-A1.
XX
PD 07-NOV-2002.
XX
PF 07-AUG-2001; 2001US-00924400.
XX
PR 11-JAN-1996; 96US-00585392.
PR 10-JAN-1997; 97WO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00391789.
PR 17-APR-1998; 98US-00062451.
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00593925.
PR 16-MAR-2001; 2001US-00810936.
XX
(FRUD/) FRUDAKIS T N.
PA (REED/) REED S G.
PA (SMITH/) SMITH J M.
PA (MISH/) MISHNER L E.
PA (DILL/) DILLON D C.
PA (RETT/) RETTER M W.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HARL/) HARLOCKER S L.
PA (DAYC/) DAY C H.
PA (LISX/) LI S X.
PA (DENG/) DENG T.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
XX
WPI: 2003-247262/24.
XX
P-PSDB; ADAL1394.
XX
PT New breast tumor proteins nucleic acids encoding such proteins, useful in
PT diagnosing, preventing and/or treating diseases such as cancer,
PT particularly breast cancer, and as markers for detecting the presence of
PT a cancer.
XX
PS Claim 1; Page 149; 190pp; English.
XX
CC The invention relates to a breast tumour polynucleotide selected from one
CC of the 275 fully defined nucleotide sequences (a) given in the
CC specification, including their complements, sequences consisting of at
CC least 20 contiguous residues of a sequence in (a), sequences that
CC hybridise to a sequence in (a) under moderately stringent conditions,
CC sequences having at least 75% or 90% identity to a sequence in (a), or
CC degenerate variants of a sequence in (a). Also included are an isolated
CC polypeptide (ii) comprising an amino acid sequence selected from
CC sequences encoded by (a), sequences having at least 70% or 90% identity
CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
CC sequences (c), and sequences having at least 70% or 90% identity to a
CC sequence in (c), expression vectors comprising (a), a host cell
CC transformed or transfected with the expression vector, an isolated
CC antibody or its antigen-binding fragment that specifically binds to (ii),
CC a method for detecting the presence of a cancer in a patient, a fusion
CC protein comprising at least one polypeptide (ii), an oligonucleotide that
CC hybridises to (a), under moderately stringent conditions, a method for
CC stimulating and/or expanding T cells specific for a tumour protein (by

CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii)), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 89.2%; Score 831.8; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 1.4e-238;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
DB 42 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101
QY 159 GACGCTTGGAGCAAGAGCTGCAAGTGGTCTGCCACTGCTTCCCTGTGAGGGGGAG 218
DB 102 GACGCTTGGAGCAAGAGCTGCAAGTGGTCTGCCACTGCTTCCCTGTGAGGGGGAG 161
QY 219 CGGCAAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCAG 278
DB 162 CGGCAAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCAG 221
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DB 222 GTACCAAGCTCCATGGAGAGATCTGGCAAGCTCCACAGAGCTGCTGTGGGTAAAGT 281
QY 339 CCCGAGAAAGATCTATCTGCTATGCTCAGGACACTGATGTAACAAGAGGACAGCA 398
DB 282 CCCGAGAAAGATCTATCTGCTATGCTCAGGACACTGATGTAACAAGAGGACAGCA 341
QY 399 AAGAGAGCTGCTTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTCGT 458
DB 342 AAGAGAGCTGCTTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTCGT 401
QY 459 GCTGGACAGACGATGTCAACTTAATGCTTGTGACCAACAAAGAGACAGCTCTGACAA 518
DB 402 GCTGGACAGACGATGTCAACTTAATGCTTGTGACCAACAAAGAGACAGCTCTGACAA 461
QY 519 GGCGGTACATGCCAGAGCAAGTGAATGCTGTTAATGCTTGGACATGGCACTGATCC 578
DB 462 GGCGGTACATGCCAGAGCAAGTGAATGCTGTTAATGCTTGGACATGGCACTGATCC 521
QY 579 AAATATTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAATGAATAA 638
DB 522 AAATATTCCAGATGAGTATGGAATACCACTTACACTATGCTGTCTACAAATGAATAA 581
QY 639 ATTAATGCCAAGACACTGCTTATACGCTGCTGATATCGATCAAAACAGCATGG 698
DB 582 ATTAATGCCAAGACACTGCTTATACGCTGCTGATATCGATCAAAACAGCATGG 641
QY 699 CCTCACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
DB 642 CCTCACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAACCGAATTTAAATGGCGCTGGATAGTATGGAAGAACTGCTCTCATCTGC 818
DB 702 CAAGAAAACCGAATTTAAATGGCGCTGGATAGTATGGAAGAACTGCTCTCATCTGC 761
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCGCTCTACTTGGCAAAATGCTGATGATC 878
DB 762 TGTATGTTGGATCAGCAAGTATAGTCAGCGCTCTACTTGGCAAAATGCTGATGATC 821

QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
DB 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 15

ADCI5366

ID ADCI5366 standard; DNA; 879 BP.

XX ADCI5366;

AC ADCI5366;

XX 18-DEC-2003 (first entry)

XX Human breast tumour protein DNA, SEQ ID 314.

XX Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;

XX ds.

XX Homo sapiens.

XX WO2003013431-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024917.

XX 07-AUG-2001; 2001US-00924400.

XX 20-FEB-2002; 2002US-00079137.

XX 02-AUG-2002; 2002US-00212679.

XX (CORI-) CORIXA CORP.

XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;

XX Kalos MD;

XX WPI; 2003-342398/32.

XX New polynucleotide, useful for preparing a composition for diagnosing,

XX treating or preventing cancer.

XX Example 1; SEQ ID NO 314; 308pp; English.

XX The present invention relates to compositions and methods for the therapy

XX and diagnosis of cancer, particularly breast cancer. The method for

XX detecting the presence of a cancer in a patient comprises: obtaining a

XX biological sample from the patient; contacting the biological sample with

XX a binding agent that binds to the polypeptide; detecting in the sample an

XX amount of the polypeptide that binds to the binding agent; and comparing

XX the amount of the polypeptide to a predetermined cut-off value. Treating

XX breast cancer comprises administering a composition comprising breast

XX tumour proteins and nucleic acids, which simulates and/or expands T cells

XX specific for the tumour protein. The present sequence was used to

XX illustrate the invention.

XX Query Match 89.2%; Score 831.8; DB 9; Length 879;

XX Best Local Similarity 99.8%; Pred. No. 1.4e-238;

XX Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158

DB 42 CAGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 101

QY 159 GACGCTTGGAGCAAGAGTGAAGTGGTGTGCTGCCACTGCTTCCCTGTGAGGGGGAG 218

DB 102 GACGCTTGGAGCAAGAGTGAAGTGGTGTGCTGCCACTGCTTCCCTGTGAGGGGGAG 161

QY 219 CGGCAAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCAG 278

DB 162 CGGCAAGCAAGCTGGGCGCTTGGGAGACTAGATGACAGCGCTTCTATGATCCAG 221

Qy	279	GTACCACGTCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGTAAAGT	338
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Qy	339	CCCCAGAAAGGATCTCATGGTCATCCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA	398
Db	282	CCCCAGAAAGGATCTCATGGTCATCCTCAGGGACACTGATGTGAACAAGAGGGACAAGCA	341
Qy	399	AAAGAGGACTGCTCTACATCTCGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT	458
Db	342	AAAGAGGACTGCTCTACATCTCGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCGT	401
Qy	459	GCTGGACAGACGATGTCAACTTTAATGTCTTGCACCAACAAAAAGAGGACAGCTCTGACAAA	518
Db	402	GCTGGACAGACGATGTCAACTTTAATGTCTTGCACCAACAAAAAGAGGACAGCTCTGACAAA	461
Qy	519	GGCCGTACAAATGCCAGGAGATGATGTCGTTAATGTCTGGAAACATGGCAGCTGATCC	578
Db	462	GGCCGTACAAATGCCAGGAGATGATGTCGTTAATGTCTGGAAACATGGCAGCTGATCC	521
Qy	579	AAATATTCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA	638
Db	522	AAATATTCAGATGAGTATGGAAATACCACTCTACACTATGCTGTCTACAATGAAGATAA	581
Qy	639	ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGATCGAATCAAAAAACAGCATGG	698
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Qy	699	CCTCACACCACTGCTACTTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT	758
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Qy	759	CAAGAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGACTGCTCTCATCTTGC	818
Db	702	CAAGAAAAAGCGAATTTAAATCGCTGGATAGATATGGAAGACTGCTCTCATCTTGC	761
Qy	819	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAAATGTTGATGATC	878
Db	762	TGTATGTTGTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAAATGTTGATGATC	821
Qy	879	TTCTCAAGATCTGGAAGACGGCCAGAGATATGCTGTTTCTAGTCATCATG	933
Db	822	TTCTCAAGATCTGGAAGACGGCCAGAGATATGCTGTTTCTAGTCATCATG	876

Search completed: April 30, 2004, 11:22:37
Job time : 430 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 11:07:17 ; Search time 2524 Seconds
(without alignments)
11038.595 Million cell updates/sec

Title: US-10-079-137b-343

Perfect score: 933

Sequence: 1 atggtgttgagggtgattc.....tggttttagtcatcatg 933

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	541	58.0	621	12	BM763942 K-EST0045
2	540	57.9	633	12	BM763453 K-EST0044
3	395.6	42.4	729	13	BU930826 AGENCOURT
4	390.8	41.9	865	10	BF676987 602084215

RESULT 1
BM763942

LOCUS K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-All 5',

DEFINITION mRNA sequence.

ACCESSION BM763942

VERSION BM763942.1 GI:19093557

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 621)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

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Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsungemail.kribb.re.kr

Plate: 25 row: A column: 11

High quality sequence stop: 621.

ALIGNMENTS

621 bp mRNA linear EST 04-MAR-2002
K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-All 5',
mRNA sequence.
BM763942
BM763942.1 GI:19093557
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 621)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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Fax: +82-42-860-4409
Email: yongsungemail.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.

5 376.4 40.3 505 13 BX492731 DKFZP781C
6 349.2 37.4 992 13 BX437445
7 342.4 36.7 843 9 AU120666
8 331.2 35.5 544 9 AL703938 DKFZP686E
9 315.2 33.8 1020 12 BM469654
10 274 29.4 2285 11 BC038951 Homo sapi
11 264 28.3 539 9 AA910780 cl48B04.8
12 260.8 28.0 3443 11 BC028407 Homo sapi
13 259.2 27.8 1079 12 BM548157 AGENCOURT
14 256.8 27.5 754 13 BU568215 AGENCOURT
15 253.6 27.2 750 12 BU871077
16 249.6 26.8 1961 11 AK087771 Mus muscu
17 249.2 26.7 537 12 BM511319 iJ46C10.Y
18 248 26.6 1347 11 AK084890 Mus muscu
19 248 26.6 1758 11 AK017783
20 227.6 24.4 380 10 BF323652 RC6-BN027
21 219.2 23.5 956 13 BY171578 AGENCOURT
22 217.6 23.3 802 13 BQ432733 AGENCOURT
23 214 22.9 958 12 B1828139
24 214 22.9 1025 12 BM554194
25 213 22.8 747 12 BG171440
26 211 22.6 748 12 B1831866
27 210.2 22.5 810 12 BG703856
28 208.4 22.3 802 13 BU853535
29 208.4 22.3 856 12 B1830348
30 208 22.3 907 12 BG721483
31 207.6 22.3 743 12 B1826430
32 206.8 22.2 828 12 B1827177
33 206.8 22.2 1558 12 BM559510 AGENCOURT
34 206.4 22.1 781 12 B1560539
35 206.2 22.1 808 12 B1549417 60374383
36 206 22.1 864 12 B1831391
37 204.6 21.9 916 12 BG716974 602689005
38 203.2 21.8 830 12 B1520473 603071669
39 202.4 21.7 899 12 B1546858 603189764
40 202.2 21.7 1854 11 AK015948
41 200.8 21.5 755 13 BU852757
42 200.8 21.5 845 13 BU569542
43 199.2 21.4 694 12 BG720647
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FEATURES

Source Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-25-A11"
 /tissue-type="myeloma"
 /cell_line="KMS-5"
 /lab_hosts="Top10F"
 /clone_lib="S13KMS5"
 /note="vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dr-selected mRNA by priming with dr-tailed vector. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 58.0%; Score 541; DB 12; Length 621;
 Best Local Similarity 100.0%; Pred. No. 1.6e-125; Indels 0; Gaps 0;
 Matches 541; Conservative 0; Mismatches 0;
 QY 393 CAAGCAAAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 452
 DB 1 CAAGCAAAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 60
 QY 453 ACTGCTCTGGACAGAGATGTCACACTTAATGTCCTTGCACAAACAAAGAGGACGCTCT 512
 DB 61 ACTGCTCTGGACAGAGATGTCACACTTAATGTCCTTGCACAAACAAAGAGGACGCTCT 120
 QY 513 GACAAAGCCGTCACAAAGCACTGCTCTTATACGGTGGCTGATCGAATCAAAACAA 572
 DB 121 GACAAAGCCGTCACAAAGCACTGCTCTTATACGGTGGCTGATCGAATCAAAACAA 180
 QY 573 TGATCCAAATATTCAGATGAGTATGGAATACCACTTACACTGCTCTTACAAATGA 632
 DB 181 TGATCCAAATATTCAGATGAGTATGGAATACCACTTACACTGCTCTTACAAATGA 240
 QY 633 AGATAAATTAATGGCCAAAGCACTGCTCTTATACGGTGGCTGATCGAATCAAAACAA 692
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 QY 693 GCATGGGCTCACACCACTGCTTGTATACATGAGCAAAACAGCAAGTGTGAAAT 752
 DB 301 GCATGGGCTCACACCACTGCTTGTATACATGAGCAAAACAGCAAGTGTGAAAT 360
 QY 753 TTTAATCAAGAAAAGCGAATTTAATGCGCTGGATAGATATGGAAGAACTGCTTCAT 812
 DB 361 TTTAATCAAGAAAAGCGAATTTAATGCGCTGGATAGATATGGAAGAACTGCTTCAT 420
 QY 813 ACTTGCCTGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGA 872
 DB 421 ACTTGCCTGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTGGAGCAAAATGTTGA 480
 QY 873 TGTATCTTCTCAAGATCTGGAACCGCCAGAGAGTATGCTTTTCTAGTCATCATCAT 932
 DB 481 TGTATCTTCTCAAGATCTGGAACCGCCAGAGAGTATGCTTTTCTAGTCATCATCAT 540
 QY 933 G 933
 DB 541 G 541

RESULT 2

BM763453
 LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5' linear EST 04-MAR-2002
 DEFINITION mRNA sequence.
 ACCESSION BM763453
 VERSION BM763453.1 GI:19093069
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 633)
 AUTHORS Oh,K.N., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Kim,Y.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 High quality sequence stop: 633.

FEATURES

Location/Qualifiers
 1. 633
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /tissue-type="myeloma"
 /cell_line="KMS-5"
 /lab_hosts="Top10F"
 /clone_lib="S13KMS5"
 /note="vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dr-selected mRNA by priming with dr-tailed vector. The dr-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 57.9%; Score 540; DB 12; Length 633;
 Best Local Similarity 99.8%; Pred. No. 2.8e-125;
 Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 393 CAAGCAAAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 452
 DB 1 CAAGCAAAAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAA 60
 QY 453 ACTCGTGTGGACAGACGATGTCACACTTAATGTCCTTGCACAAACAAAGAGGACGCTCT 512
 DB 61 ACTCGTGTGGACAGACGATGTCACACTTAATGTCCTTGCACAAACAAAGAGGACGCTCT 120
 QY 513 GACAAAGCCGTCACAAATCCAGGAAGATGATGCGTTAATGTTGCTGGACATGGCAC 572
 DB 121 GACAAAGCCGTCACAAATCCAGGAAGATGATGCGTTAATGTTGCTGGACATGGCAC 180
 QY 573 TGATCCAAATATTCAGATGAGTATGGAATACCACTTACACTATGCTGTCTCAATGA 632

Db 181 TGATCCAAATATCCAGATGAGTGAATACCACTCTACACTATGCTGTCTACAATGA 240
 QY 633 AGATAAATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAA 692
 Db 241 AGATAAATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAA 300
 QY 693 GCATGGGCTCACACACTGCTTACTTGTATACATGAGCAAAAAACAGCAAGTGTGAATT 752
 Db 301 GCATGGGCTCACACACTGCTTACTTGTATACATGAGCAAAAAACAGCAAGTGTGAATT 360
 QY 753 TTTAATCAAGAAAAAGCAATTTAAATGCGCTGGATAGATAGAAAGAACTGCTTCAT 812
 Db 361 TTTAATCAAGAAAAAGCAATTTAAATGCGCTGGATAGATAGAAAGAACTGCTTCAT 420
 QY 813 ACTTGCTGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGCAGCAAAATGTTGA 872
 Db 421 ACTTGCTGTATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGCAGCAAAATGTTGA 480
 QY 973 TGTATCTTCTCAAGATCTGGAAGACGCCAGAGAGATGCTGTTCTAGTCATCATCAT 932
 Db 481 TGTATCTTCTCAAGATCTGGAAGACGCCAGAGAGATGCTGTTCTAGTCATCATCAT 540
 QY 933 G 933
 Db 541 G 541

RESULT 3
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 LOCUS AGENCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
 DEFINITION 5', mRNA sequence.
 ACCESSION BU930826
 VERSION BU930826.1 GI:24119645
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA distribution: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 High quality sequence stop: 555.
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 /db_xref="taxon:9606"
 /clones="IMAGE:6668956"
 /lab_host="DH10B (T1 phage-resistant)"
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 /note="Organ: prostate; Vector: pDNR-LTB (Clontech); Site1: SfII (ggcgctcgccg); Site2: SfiI (ggccatagggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

FEATURES

source
 1..729
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:6668956"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 83"
 /note="Organ: prostate; Vector: pDNR-LTB (Clontech); Site1: SfII (ggcgctcgccg); Site2: SfiI (ggccatagggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 42.4%; Score 395.6; DB 13; Length 729;
 Best Local Similarity 90.5%; Pred. No. 8.9e-89;
 Matches 458; Conservative 0; Mismatches 14; Indels 34; Gaps 2;
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 Db 3 GGACAGAGCATGCTCAACTTAATGCTCTTACAAACAAAAGAGGACAGCTCTGATAAGGT 62
 QY 518 -----AGCCCGTCAAAATGCCAGGAAGATGAATGCGGTT 551
 Db 63 ATGCAGTAGCCAACTATATCAGCATGAGCGCGTCAATGCGCAGGAAGATGAATGCGGTT 122
 QY 552 AATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 611
 Db 123 AATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 182
 QY 612 ACACATATGCTGTCTCAATGAAGATAAAATTAATGCCAAAGCACTGCTCTTATACGGTGC 671
 Db 183 GCACATAGCTATCTATATGAAGATAAAATTAATGCCAAAGCACTGCTCTTATACGGTGC 242
 QY 672 TGATATCGAATCAAAAAACAGCATGGGCTCACACACTGCTTACTTGGTATACATGAGCA 731
 Db 243 TGATATCGAATCAAAAAACAGCATGGGCTCACACACTGCTTACTTGGTATACATGAGCA 302
 QY 732 AAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCGCTGTATAG 791
 Db 303 AAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCGTGTATAG 362
 QY 792 ATATGGAAGAACTGCTCTCATACTTCTGTATGTTGTGGATCAGCAAGPATAGTCAGCCC 851
 Db 363 ATATGGAAGAACTGCTCTCATACTTCTGTATGTTGTGGATCAGCAAGPATAGTCAGCCC 422
 QY 852 TCTACTTGAGCAAAATGTTGATGTATCTTCTCAAG---ATCTGGAAGACGCGCCAGAGA 907
 Db 423 TCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTATCTGGACAGACGCGCCAGAGA 482
 QY 908 GTATGCTGTTTCTAGTCATCATCATG 933
 Db 483 GTATGCTGTTTCTAGTCATCATCATG 508

RESULT 4

BF676987 865 bp mRNA linear EST 21-DEC-2000
 LOCUS 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
 DEFINITION mRNA sequence.
 ACCESSION BF676987
 VERSION BF676987.1 GI:11950882
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 865)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LiCM1067 row: m column: 03
 High quality sequence stop: 642.
 Location/Qualifiers
 1..865
 /organism="Homo sapiens"

FEATURES

source

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccctcgcc); Site 2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

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ORIGIN

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Query Match      41.9%; Score 390.8; DB 10; Length 865;
Best Local Similarity 97.4%; Pred. No. 1.6e-87;
Matches 409; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 518 AGCCGTACAAATCCAGGAGATGATGTCGTTAATGTTGTTGGAACATGCACTGATC 577
Db 69 AGCCGTACAAATCCAGGAGATGATGTCGTTAATGTTGTTGGAACATGCACTGATC 128

QY 578 CAAATATTCAGATGATGAAATACCACTTACATATGCTGTCTACATGAAGATA 637
Db 129 CAAATATTCAGATGATGAAATACCACTTACATATGCTGTCTACATGAAGATA 188

QY 638 AATTATGSCCAAGACACTGCTTTATACGGTGCTGATATCAATCAAAAAACAGCATG 697
Db 189 AATTATGSCCAAGACACTGCTTTATACGGTGCTGATATCAATCAAAAAACAGCATG 248

QY 698 GCCTCACACACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAA 757
Db 249 GCCTCACACACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAA 308

QY 758 TCAAGAAAAAGCAATTTAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTG 817
Db 309 TCAAGAAAAAGCAATTTAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTG 368

QY 818 CTGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTCAGCAAAATGTTGATGAT 877
Db 369 CTGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTCAGCAAAATGTTGATGAT 428

QY 878 CTCTCTCAAG-----ATCTGAAAGACGGCCAGAGATGCTGTTTCTAGTCATCATG 933
Db 429 CTCTCTCAAGATCTATCTGACAGACGGCCAGAGATGCTGTTTCTAGTCATCATG 488

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RESULT 5
BX492731
LOCUS      505 bp mRNA linear EST 04-SEP-2003
DEFINITION DKF2p781C0523 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
            DKF2p781C0523 5', mRNA sequence.
ACCESSION  BX492731
VERSION     BX492731.1 GI:32004516
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 505)
AUTHORS    Bloeker, H., Boecker, M., Meves, H.W., Weil, B., Amid, C., Oanger, A.,
            Pobo, G., Han, M. and Wiemann, S.
TITLE      EST (Bloeker, H., Boecker, M., Meves, H.W., Weil, B., Amid, C., et al.)
JOURNAL    Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

```

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.

No 51 sequence available.

This clone (DKF2p781C0523) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES

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source
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p781C0523"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: hlcc4)"
/note="vector: pSport1_Sfi; Site_1: SfiA; Site_2: SfiB;
cDNA-collection"

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ORIGIN

```

Query Match      40.3%; Score 376.4; DB 13; Length 505;
Best Local Similarity 92.7%; Pred. No. 5.2e-84;
Matches 395; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 208 TGCAAGGGGAGCGGCAAGACAACTGGGCGCTTGGGGAGACTACGATGACAGCGCTTC 267
Db 80 TGGCTGGGAGCGGCAAGACAACTGGGCGCTTGGGGAGACTACGACGACGCGCTTC 139

QY 268 ATGGATCCGAGGTACCACTGTCATGGAGAGATCTGGCAAGCTCCACAGAGTGCCTGG 327
Db 140 ATGGAGCCGAGGTACCACTGTCGCGTCCGAGAGATCTGGCAAGCTCCACAGAGTGCCTGG 199

QY 328 TGGGGTAAAGTCCCGAGAAAGGATCTCATCTGTCAGGGACACTGATGTGAACAAG 387
Db 200 TGGGGTAAAGTCCCGAGAAAGGATCTCATCTGTCGGGGACACCGACCTGAGCGTG 259

QY 388 AGGACAAGCAAAAGAGGACTGCTTACATCTGGGCTCTGCCAATGGGAATTCAGAAGTA 447
Db 260 AGGACAAGCAAAAGAGGACTGCTTACATTTGGGCTCTGCCAATGGGAATTCAGAAGTA 319

QY 448 GTAAATCTGCTGGACAGACGATGTCAATTAATGTCCTTCACCAACAAAAAGAGACA 507
Db 320 GTAAATCTGCTGGACAGACGATGTCAATTAATGTCCTTCACCAACAAAAAGAGACA 379

QY 508 GCTCTGCAAAAGCGGTACAAATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACAT 567
Db 380 GCTCTGATAAAGCGGTACAAATGCCAGGAAGATGATGTTGTTAATGTTGCTGGAACAT 439

QY 568 GGCACTCATCAATATTCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTAC 627
Db 440 GGCGCTGATGGAATATTCAGATGAGTATGGAATACCGCTCTACACTATGCTGTCTAC 499

QY 628 AATGAA 633
Db 500 AATGGA 505

```

RESULT 6

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BX437445
LOCUS      992 bp mRNA linear EST 15-MAY-2003
DEFINITION BX437445 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006YL04
            5-PRIME, mRNA sequence.
ACCESSION  BX437445
VERSION     BX437445.1 GI:30771569
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 992)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization

```

JOURNAL
COMMENT

Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5500.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0CAP006DF02P1&cluster=5500.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0CAP006DF02P1.

FEATURES
source

Location/Qualifiers
1. .992
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP006Y104"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 37.4%; Score 349.2; DB 13; Length 992;
Best Local Similarity 68.9%; Pred. No. 5.5e-77;
Matches 496; Conservative 1; Mismatches 214; Indels 9; Gaps 1;

QY 106 AGCGGCAAGAGCAAGCTGGGCACTCTGGAGACCAACAGCTCTCTGTGAGAGCGTT 165
Db 182 AGAGCCGAGAGACATGAGGTCTCTGAGCCGGTCTGCTGGGCCATGAAGAGATT 241
QY 166 GGAGCAAGAGTGCAGTGGTGTCTGCCACTCTTCCCTGTGCGAGGGGAGCGCAAG 225
Db 242 TTATGTAAGAAAGGCGAGTCGCCCTTGGCTCTCTCGC-----GCGGCGGGAGG 292
QY 226 AGCAAGCTGGCGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCAGGTACCAC 285
Db 293 AGCAGCGCGGAGCGGGGCGGAGCGGGGAGGGCGCTTCTGAGCGCCCGGTACCAC 352
QY 286 GTCCATGAGAGAGATCGGACAGCTCCACAGAGCTGCTGTGGGTAAAGTCCGCCAGA 345
Db 353 GTCCGAGCCGAGATCTCGCAAGATCCACAAAGCTGCCAGCGGGTAATGTGGCGAA 412
QY 346 AAGATCTCATGCTATGCTCAGGACACTGATGTGAACAAGAGGACAGCAAAAGAGG 405
Db 413 GTGACGAGATCTTTTGTCTAGGAAGATGCTTGAACGATAGAGCAAGATGAACAGG 472
QY 406 ACTGCTCTACATCTGCGCTCTGCCAATGGGAATTCAGAAAGTAGTAATAAAGTCTGCTGGAC 465
Db 473 ACGGCTCTACATTTGGCTTGGCCATGTCTATCAGAAAGTAGTAATAAAGTCTGCTGGAC 532
QY 466 AGAGATGTCAACTTAATGTCTTGAACAACAAAGAGGACAGCTTGCACAAAGCCGTA 525
Db 533 AGAAATGCGCAGTCAATGCTGTGACAAACGAAACAGGACAGCTCTGATGAAGCTGTA 592
QY 526 CAATGCCAGAGATGAATGCGTTAATGTGTGGACATGGCACTGATCCAAATATT 585
Db 593 CAATGCCAGAGAGAAATGTGCAACTATCTGTAGAACATGGTGTGATCCAAATCTT 652
QY 586 CCAGATGAGTATGGAATACCACTCTACACTATGCTGTCTACAAATGAAGATAAATATG 645
Db 653 GCGGATGTCATGGCAACACTGCTCTTCACTATGCTGTCTATAATGAGGACATATCAGTA 712
QY 646 GCCAAGCACTGCTCTTATACGGTGTGATTCGAATCAAAAACAGCATGGCTCACA 705
Db 713 GCAACAAAGCTGCTTTTGTATGATGCAATATATGAGCAAAAACAGGATGACCTACA 772
QY 706 CCAGTCTACTTGGTATATCATGAGCAAAAACAGCAAGTGTGTAATTTAATCAAGAA 765

Db 773 CCACCTTTTACTTGCAGTAAGTGAARAGCAGCAATGGTGGTAATTTTAAATAGAAA 832
QY 766 AAAGCGAATTTAAATGCGCTGGATAGATATGAGAACTGCTCTCATACTTCTGTATGT 825
Db 833 AAAGCAATGTAATGTCAGTGGTAAGTTGGAAGAGCTACCAACTAATTTTCAAGATAT 892

RESULT 7

AUI20666
LOCUS AUI20666 HEMBB1 Homo sapiens cDNA clone HEMBB1001175 5', mRNA
DEFINITION sequence.
ACCESSION AUI20666
VERSION AUI20666.1 GI:10935901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 843)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986

TITLE
JOURNAL
COMMENT

Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1001175"
/tissue_type="whole embryo, mainly body"
/dev stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"

FEATURES
source

Query Match 36.7%; Score 342.4; DB 9; Length 843;
Best Local Similarity 68.6%; Pred. No. 2.6e-75;
Matches 488; Conservative 0; Mismatches 214; Indels 9; Gaps 1;

ORIGIN

QY 106 AGCGGCAAGAGCAAGCTGGGCACTCTGGAGACCAACAGCTCTCTGTGAAGAGCGTT 165
Db 119 AGAGCCGAGAGACATGAGGTCTCTGAAAGCCCGCTCGCCCTGAGAGAGATT 178
QY 166 GGGAGCAAGAGTGTGCTGCTGCCACTGCTTCCCTGTCTGCGGGGAGCGGCAAG 225
Db 179 TTATGTAAGAAAGGCGAGTCGCCCTTGGGTCTCTCGC-----GCGGCGGGAGG 229
QY 226 AGCACTGTGGCGCTTGGGAGACTACGATGACAGCGCTTCTGATCCAGGTACCAC 285
Db 230 AGCAGCGCGGAGCGGGGCGGAGCGCGGGGAGCGGCGCTTCTCGAGCGCGGTACCAC 289
QY 286 GTCCATGAGAGATCTGGACAAGCTCCACAGAGCTGCTTGGGTAAAGTCCCCAGA 345
Db 290 GTCCGAGCCGAGATCTGCGCAAGATCCCAAGCTGCGAGCGGGTATGTGGCGAAA 349
QY 346 AAGATCTCATGCTCATGCTCAGGACACTGATGTGAACAAGAGGGGACAAAGAGAGG 405
Db 350 GTGACGAGATCTCTTTTGTCTCAGGAAGATGGCTTGAACCGATAGACAGATGACAGG 409

QY	406	ACTGCTTACATCTCGCCTCTGCCAATGGGAATTCAGAAGTAGTAAACCTCGTGTGGAC	465
Db	410	AGGGCTTACATTGGCCCTGTGCCAATGGTCATCCAGAAGTAGTAACTCTCTGTGGTGCAC	469
QY	466	AGACGATGTCACATTAAATGCTCTTGACACACAAAAGAGGACAGCTCTGCACAAAGCCGTA	525
Db	470	AGAAATGCCAGCTCAATGTCTGTGACACAGAAACAGGACAGCTCTGTATGAAGCGCTGA	529
QY	526	CAATGCCAGGAAGATGGAATGTGCGCTTAATGTGCTGGAACATCGGCACCTGATCCAAATATT	585
Db	530	CAATGCCAGGAAGAGAATGTGCAACTATTCTGCTAGAACATGGTGCTGATCCNAATCTT	589
QY	586	CCAGATGAGTATGGAATAACCACTCTACACTATGCTCTCTACAAATGAAGATAAATTAATG	645
Db	590	GCGGATGTCATGGGCAACACTGCTCTTCACTATGCTCTATTATGAGGACATATCAGTA	649
QY	646	GCCAAAGCACCTGCTTTATACGGTGTGATATCGAATCAAAAACCAAGCATGGCCTCACA	705
Db	650	GCAACAAGCTGCTTTGTATGATGCAAAATTGAAGCAAAAACCAAGGATGACCTNACA	709
QY	706	CCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGGTGAATTTTTTAAATCAAGAAA	765
Db	710	CCACTTTTACTTGCAGTAAGTGGAAAAAAGCAGCAATGGTGGAAATTTTTTAATAAAGAAA	769
QY	766	AAAGCGAATTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTT	816
Db	770	AAAGCAAAATGTAAAGCCNTANATAAGTTGGAAGCAGTCACCACTAAATTT	820

RESULT 8	AL703938	544 bp	linear	EST 04-SEP-2003
LOCUS	DFXZP686B1728	rl 686 (synonym: hlccs)	Homo sapiens	cDNA clone
DEFINITION	DFXZP686B1728 5', mRNA sequence.			
ACCESSION	AL703938			
VERSION	AL703938.1	GI:19687293		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Ottewaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and Wiemann,S.			
TITLE	EST (Ottewaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann,S.)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: MIPS			
	MIPS			

This clone (DKFZp686E1728) is available at the KZPD in Berlin. Please contact the KZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clones@kzpd.de.

```

FEATURES
source
1.544
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686E1728"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="696 (synonym: hlcc3)"
/note="vector: pTriplex2; Site_1: SfiI; Site_2: SfiI; cDNA-Collection"

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CLNA-COLLECTION	ORIGIN	Query Match	Score	DB	Length
		35.5%	331.2	9	544

	Best Local Similarity Matches	91.9%; 373; Conservative	Pred. No. 1.4e-72; 0; Mismatches	28; Indels	5; Gaps	2;
QY	532	CAGGAAGATGAATGTGGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATTCCAGAT	591			
Db	1	CAGGAAGATGAATGTGTGTTAAATGTTGCTGGAAACATGGCGCGATGGAAATATTCAAGAT	60			
QY	592	GAGTATGGAATACCACTCTACACTATGCTGTCTACAATGAAGATAAAATTAAATGCCAAA	651			
Db	61	GAGTATGGAATACCGCTCTACACTAT - CTATCTCATGTAAGNTAAATTTAATGGCCAAA	119			
QY	652	GCATGCTCTTTATACGGTGTGTATTCGAATCAAAAAACAAGCATGGGCTCACACCATG	711			
Db	120	GCATGCTCTTTATGTGTGTATTAATCAAAAAACAAGTGTGGCTCACACCATTT	179			
QY	712	CTACTTGGTATACATGAGCAAAAACAAGCAAGTGGTGAATTTTAACTCAAGAAAAAGCG	771			
Db	180	TTGCTTGGCGTGCATGAACAAAAACAAGGAAGTGGTGAATTTTAACTCAAGAAAAAGCT	239			
QY	772	AATTTAAATGGCTGGATACATATAGNAGAACTGCTCTCATACTGCTGTATGTTGGGA	831			
Db	240	AATTTAAATGACCTTGATATAGATATGGAAGAACTGCCCTCATACTTGTCTGTATGTTGGGA	299			
QY	832	TCAGCAAGTATAGTCGCCCTCTACTTTGAGCAAAATGTTGATGATCTTCTCAAG - - - A	887			
Db	300	TCAGCAAGTATATCATCTCTTACTTTGAGCAAAATGTTGATGATCTTCTCAAGATCTA	359			
QY	888	TCTGAAAGCGGCCAGAGATATGCTGTTTCTAGTCATCATCATG	933			
Db	360	TCTGGAACAGCGGCCAGAGATATGCTGTTTCTAGTCATCATCATG	405			

RESULT 9	
BM469654	
LOCUS	linear
DEFINITION	1020 bp mRNA
	AGNCOURT_6444673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
	5', mRNA sequence.
ACCESSION	BM469654
VERSION	BM469654.1
KEYWORDS	GI:18518696
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (Bases 1 to 1020)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

```

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgpabs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12351 row: m column: 06
High quality sequence stop: 680.
Location/Qualifiers
1..1020
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5585453"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH103 (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
FEATURES
source

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ORIGIN

Query Match 33.8%; Score 315.2; DB 12; Length 1020;
 Best Local Similarity 73.7%; Pred. No. 2.1e-66;
 Matches 401; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 282 CCAGTCCATGGGAGAGATCTGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCC 341
 Db 1 CCAGTCCGAGACGAGATCTGCGCAAGATCCCAAGCTGCCAGCGGGTAATGTGGC 60

Qy 342 CAGAAAGATCTCATCTGCTCAGGACATGATGTAACAAGAGGACAGCAAA 401
 Db 61 GAAAGTCAGCAGATCTTTTGTCTGAGAAAGATGGCTTGAACGATAGACAGATGAA 120

Qy 402 GAGGACTGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461
 Db 121 CAGACGGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 462 GGACAGAGATGTCATCTTAATGCTCTGACCAAAAGAGACAGCTCTGCAAGGC 521
 Db 181 GGACAGAAATGCCAGCTCAATGCTGACACGAAACAGGACAGCTCTGATGAAGC 240

Qy 522 CGTCAATGCCAGAGATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
 Db 241 TGTCAATGCCAGAGAGAAATGCACTATTCTCTAGAACATGCTGCTGCTGCTCAA 300

Qy 582 TATTCAGATGATGGAATATCACTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
 Db 301 TCTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

Qy 642 AATGCCAAGACATGCTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
 Db 361 AGTAGCAACAAAGCTGCTTGTATGATGCAATATTGAAAGCAAAACAGGATGACCT 420

Qy 702 CACACCACTGCTACTTGTGTATACATGACCAAAACAGCAAGTGGTGAATTTTATCAA 761
 Db 421 CACACCACTTTTACTTCAGTAAAGTGAAGAAAGACCAATGCTGGAATTTTATCAA 480

Qy 762 GAAAGAGCAATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821
 Db 481 GAAAGAGCAATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Qy 822 ATGT 825
 Db 541 ATAT 544

RESULT 10
 BC038951
 LOCUS
 DEFINITION Homo sapiens ankyrin repeat domain 19, mRNA (cDNA clone IMAGE:5733799), with apparent retained intron.
 ACCESSION BC038951
 VERSION BC038951.1 GI:25058320
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2285)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Narusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Tishiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzay, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerf, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2285)
 Strausberg, R.
 Direct Submission
 Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hgri.nih.gov

Akter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dierich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 82 Row: i Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomScan gene prediction
 This clone has the following problem: retained intron.

FEATURES

source

1..2285

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/note="Vector: pCMV-SPORT6"

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 Best Local Similarity 63.6%; Pred. No. 8.2e-58;
 Matches 435; Conservative 0; Mismatches 245; Indels 4; Gaps 1;

Qy 247 GACTACGATGACAGCGCTTCATGATCCGATCCAGTACCAGCTCCATGGAGAGATCTGGAC 306
 Db 103 GACTCCATGGACCAAGAGTAGCTGGTGGGGGTACCACATCCGGGACTGGGACTGGCG 162

Qy 307 AAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGGATCTCATGCTCATGCTC 366
 Db 163 AGATCCACAGGCTGCCATCAAGGCGCGCGGAGGTGGACACTGCCTGACGCGC 222

Qy 367 AGGACACTGATGTGAACAGAGGAGGACAGCAAGAGAGACTGCTCTACATCTGGCTCT 426
 Db 223 AGGTTCCGGGACTTGGACGCCGCCGACAGAAAGACAGGACTGTTCTCATTTGACCTGT 282

Qy 427 GCCAATGGGAATTCAGAAAGTAGTAAATTCGTGCTGGACAGACGATGTCAACTTAATGTC 486

Db 283 GCCATGGCGGTGGAGTGGTCAACCTTTCTGCTGAGCAGAGATGCCAGATCAACATA 342
QY 487 CTTGACACAAAAGAGAGCAGCTCTGACAAAGCGGTACATGCCAGGAAGATGAT 546
Db 343 TATGATAGACTAAACAGGACACCTTTTAATGAAGCTGTACACTGCCAGGAAGGCTTGT 402
QY 547 GCCTTAATGTGTGGAAATGCGACCTGATCCAAATATTCCAGATCAGTATGGAATACC 606
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QY 607 ACTCTACACTATGCTGTCTACATGAAGATAAATTAATGGCCAAAGCACTGCTCTATAC 666
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QY 667 GGTGCTGATATCAATCAAAAACAGCAGTGGCTCACACCACTGCTACTTGTGTATACAT 726
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Db 583 TCTAGGAGACAGCAAAATTTGTGAATTTCTGTTGAAGAACCCAGGCAAAATTTACATGCCAT 642
QY 787 GATAGATATGGAAGACTGCTCATACTTGTGTATGTTGTGATCAGCAGCAATAGTC 846
Db 643 GACAAATTCAGAGAACAGCCCTCATGCTTGCAGTACAGTAACTCATCAAGTATCGTC 702
QY 847 AGCCCTTACTTGAGCAAAATGTTGATGATCTTCTCAAGA----TCTGAAAGACGGCC 902
Db 703 AGCCTCCTCTTCAACAAATATAATATCTTTTCTCAAGACCTGTTTGGCAGACTGCC 762
QY 903 AGAGAGTATGCTGTTTCTAGTCAT 926
Db 763 GAGGATTATGCTGTTTGTATAAT 786

RESULT 11
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LOCUS
DEFINITION
O148b04.81 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1526671 3' Similar to TR:Q92527 Q92527 ANKYRIN MOTIF. 1, mRNA
sequence.
ACCESSION
AA910780
VERSION
AA910780.1 GI:3050070
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1548 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 235.
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/db_xref="taxon:9606"
/clone="IMAGE:1526671"
/lab_hosts="DHL10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 28.3%; Score 264; DB 9; Length 539;
Best Local Similarity 72.4%; Pred. No. 1.3e-55;
Matches 356; Conservative 0; Mismatches 135; Indels 1; Gaps 1;
QY 242 GGGGAGACTACGATCAGACAGCGCCCTTCTGATCCAGTACCGCTACCGCTCATGGAGAATC 301
Db 41 GGGGCGAGCCGGGGAGGGCGCCTTACTCGCAGCCCGCTACCACTCCGAGCCGAGATC 100
QY 302 TGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCCAGAAAGATCTCATCTCA 361
Db 101 TCGGCAGATCCACAAAGCTCCAGCGCGGGTAATGTGGCGAAAGTGCAGCAGATCCTTT 160
QY 362 TGCTCAGGCACTGATGTGAACAAGAGGAGCAAGCAAGAGAGGAGCTGCTTACATCTGG 421
Db 161 TGCTCAGAAAGATGGCTTGAACGATAGACACAGATGACAGGCGCTCTCATTTGG 220
QY 422 CCTCTGCAATGGGAATTCAGAACTAGTAAACTGCTGTGGACAGAGATGTCAACTTA 481
Db 221 CCTGTG-CAATGCTCATCCAGAGTAGTAATCTCTCTGTGGACAGAAATGCCAGTCA 279
QY 482 ATGCTCTTGACAAACAAAAGAGGAGCAGCTGTGACAAAGGCGCGTACAAATGCCAGGAAGATG 541
Db 280 ATGCTGTGACACGAAACAGGACAGCTCTGATGAGGCTGTACATGCCAGAGAGAGA 339
QY 542 AATGTCGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTTCAGATCAGATGGA 601
Db 340 AATGTGCAACTATTCTGCTAGAACATGCTGATCCAAATCTTTCGGATCTCCATGSCA 399
QY 602 ATACCACTCTACACTATGCTGCTACATGAAGATAAATTAATGCCAAAGCACTGCTCT 661
Db 400 ACATGCTCTTCACTATGCTGCTCTATATAGGACATATCAGTAGCAACAAGTGTCTT 459
QY 662 TATACGCTGCTGATATCGAATCAAAAAACAGCATGCGCTCACACCACTGCTATTGTA 721
Db 460 TGTATGATGCAATATTGAAGCACAACACAGGATGACCTCACACCACTTTTACTTGCA 519
QY 722 TACATGACGAAA 733
Db 520 TAAGTGGAAAAA 531

RESULT 12
BC028407 3443 bp mRNA linear HTC 25-NOV-2003
LOCUS
DEFINITION
Homo sapiens breast cancer antigen NY-BR-1.1, mRNA (cDNA clone
IMAGE:4821910), containing frame-shift errors.
ACCESSION
BC028407
VERSION
BC028407.1 GI:22382096
KEYWORDS
HTC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3443)
AUTHORS
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heise, P.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.W., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carrinco, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Rahay, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 REFERENCE
 2 (bases 1 to 3443)
 TITLE
 Direct Submission
 AUTHORS
 Strausberg, R.
 JOURNAL
 NIH-MGC Project URL: <http://mgs.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbio.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 46 Row: i Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORP
 analysis
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 LOCUS
 DEFINITION
 5', mRNA sequence.
 BMS48157
 BMS48157.1 GI:18782515
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 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1079)
 AUTHORS
 NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLMI2738 row: b column: 08
 High quality sequence stop: 632.
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 (destroyed); Site 2: NotI; RNA source male hippocampus,
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 cloned (EcorV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

ORIGIN


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Best Local Similarity 63.4%; Pred. No. 3e-54;
Matches 430; Conservative 0; Mismatches 243; Indels 5; Gaps 2;

QY 247 GACTACGATCAGAGCGCTTCATGGATCCAGGTACACGCTCCATGGAGAGATCTGGAC 306
DB 114 GATCCATGACCAAGAGTAGCTGTGGTGGGGGTACACATCCGGGACTGGGAATGGG 173
QY 307 AAGTCCACAGAGCTGCTGTGGGTAAAGTCCAGAGAAAGGATCTCATCGTCATGCTC 366
DB 174 AAGATCCACAGGCTGCCATCAAGGGCGAGCGCGGAGGTGGAGCACTGCCGTGACGCG 233
QY 367 AGGACACTATGTGAACAGAGGACAGCAAAAGAGAGCTCTCTAGATCTGGGCTCT 426
DB 234 AGTTCGGGACTTGGAGCGCCCGCAGAGAAAGAGAGAGCACTGTTCTAATTGACCTGT 293
QY 427 GCCAATGGGAATTCAGAAGTAGTAAACTCGTCTGACAGAGAGTGTCAACTTAATGTC 486
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QY 547 GCGTTAATGTTGTGGAACTGACATGACATCCAAATATTCAGATGAGTATGGAATACC 606
DB 414 GCCATTATCTCTGAGACATGGCGCAATCCAAACATTAAGATATCTACAGCAACT 473
QY 607 ACTCTACATATGCTGTCTCAATGAAGATAAATTAATGSCCAAGACATGCTCTTATAC 666
DB 474 GCTCTCCATATGCTGTGTATAAAGGAGCTTCACTGGCAGAAAAAATGCTTTCCAC 533
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DB 594 TCTAGGAGACAGCAATTTGTGGAATTTCTGTGAAGAACCCAGGCAAAATTTACATGCCAT 653
QY 787 GATGATATGGAGAACTGCTCATACTGCTGTATGTTGTGATGACAGCACTATAGTC 846
DB 654 GACAATTTGAGAAAGACAGCCCTCATGCTTGACGACAGCACTAATCAATCAATATGCTG 713
QY 847 AGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGA----TCTGAAAGACGGCC 902
DB 714 AGCTCTCTCTTCAAC-AAATATAAATATCTTTCTCAGACCTGTTGGCCAGACTGCC 772
QY 903 AGAGATGATGCTGTTTCT 920
DB 773 GAGGATATGCTGTTTGT 790

RESULT 14
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DEFINITION 5', mRNA sequence.
ACCESSION BUS68215
VERSION BUS68215.1 GI:22918515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
```

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cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2856 row: o column: 07
High quality sequence stop: 643.
Location/Qualifiers
1. 760
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SfiI (ggccattcgcc); Site_2: SfiI (ggccattcgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
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ORIGIN

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Query Match      27.5%; Score 256.8; DB 13; Length 760;
Best Local Similarity 64.6%; Pred. No. 1e-53;
Matches 414; Conservative 0; Mismatches 223; Indels 4; Gaps 2;

QY 262 GCCTTCTGATCCCGAGTACACGCTCCATGGAGAAGATCTGGACAAGCTCCACAGAGCT 321
DB 72 GGTTCGCATTTCCCATTTACTACATTAACCGTATCATCTGAAGAGATCCACAGAGCT 131
QY 322 GCCTGTGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATGCTCAGGACACTGATGTG 381
DB 132 GTCTTACGTGTAACTGGAGAAACTGAA---GTACCTTCTGCTCACGTATTATGACGCC 188
QY 382 AACAGAGGGACAAGCAAAAGAGGACTCTCTACATCTGGCTCTGCGCAATGGAATTC 441
DB 189 AATAAGAGACAGAGGAAGAAAGGACTGCCCTACATTTGGCTGTGCCACTGGCAACCG 248
QY 442 GAAGTAGTAAACTCGTCTGACAGAGATGTCACTTAATGTCTTGTGACAAACAAAG 501
DB 249 GAAATGGTACATCTCTGTGTCCAGAAAGTGTGAGCTTAACTCTGCGACCGTGAAGAC 308
QY 502 AGGACAGCTCTGACAAAGCGGTCAATGCCAGGAAGATGAATGCGTTAATGTTGCTG 561
DB 309 AGGACACTCTGTATCAGGCTGTACACTGAGGAGGCTTGTGCACTCTTCTGCTG 368
QY 562 GAACATGCACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCTACACTGCT 621
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QY 682 TCAAAAAACAAGCATGGCTCACACCACTGTAATTGATATACATGAGCAAAAAACAGCAA 741
DB 489 GAATGCAGCAAGATGAATATATCAGCCACTGTTACTTGTGTGAGTCGAGAAAGTGA 548
QY 742 GTGGTGAATTTTAAATCAAG-AAAAAGCGAATTTAAATCGCTGGATAGATATGGAAG 800
DB 549 ATGTGGGAATTTTAAAGAAAAAGCAATGTAATGCCATTGATTTATCTTGGCAG 608
QY 801 AACTGCTCTCATACTGCTGTATGTTGGATCAGCAAGTAGTAGTCAGCCCTCTACTTGA 860
DB 609 ATCAGCCCTCATACTGCTGTACTCTTTGGAGANAAGATATAGTCAATCTTCTCTCA 668
QY 861 GCAAAATGTTGATGTATCTTCTCAGATCTCGAAGACGGC 901
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Db 669 GCACAAATGATGTTTCTCGAGATGTATGGAAGC 709
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BI871077
VERSION BI871077.1 GI:16044750
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 754)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12030 row: d column: 13
High quality sequence stop: 729.
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Location/Qualifiers
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/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 27.2%; Score 253.6; DB 12; Length 754;
Best Local Similarity 67.2%; Pred.No. 6.6e-53;
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DB 68 TCGTTCGTCTACCGCTTATGACATCAATAAGAGAGACAGAGAGGACCGCCCTAC 127
QY 416 ATCTGGCCTCTGCCAATGGGAATTCAGAACTGATGAAATCTCGTGGACAGACGATGC 475
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QY 476 AACTTATGCTCTGACAAACAAAGAGGACGCTCTGACAAAGGCGGTACATGCCAGG 535
DB 188 AGCTTAACCTCTGCGACCGGTGAAGACAGGACACCTCTGATCAAGCGGTGTACAACCTGAGGC 247
QY 536 AAGATGAATGTGCGTTAATGTGTCTGGAACATGGCACTGATCCAAATATTCCAGATGAGT 595
DB 248 AGGAGGCTGTGCAACTCTTCTGCTGCAAAATGGCGCGATCCAAATATTACGGATGTCT 307
QY 596 ATGGAATACACATCTACACTGTCTCTACATGAAGATAAATTAATGGCCAAAGCAC 655
DB 308 TTGGAAGGACTGCTCTGCACCTACGCTGTATATGAAGATACATCCATGATAGAAAAAC 367
QY 656 TGCTCTTATACGGTGTGATGAAATCAAAAAACAAGCATGGCCTCACACCACTGCTAC 715
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Db 368 TTCTTTCATATGTTGCAAAATATTGAAGATGCGAGGATGAATATCCGCCACTGTTCC 427
QY 716 TTGGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCGAATT 775
DB 428 TTGCTGTGAGTCABAAGAAAAGTGAATATGTTGGAATTTTATTAAAGAAAAACCAATA 487
QY 776 TAAATGCCCTGGATAGATATAGGAAGAACTGCTCTCATACTTGTCTGTATGTTGTGATCAG 835
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	733	78.6	879	6	AR278590	Sequence
3	733	78.6	879	6	AR367286	Sequence
4	733	78.6	879	6	AR400322	Sequence
5	733	78.6	879	6	AR405589	Sequence
6	733	78.6	879	6	AR433323	Sequence
7	733	78.6	879	6	AR414041	Sequence
8	733	78.6	879	6	AX200901	Sequence
9	733	78.6	879	6	AX267557	Sequence
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR261059
Sequence 531 from patent US 6321716.
AR261059
AR261059.1 GI:28071822
Unknown.
Unclassified.
1 (bases 1 to 879)
Mashiki, Z. and Harada, J.
Negative pressure control apparatus for engine mounted in vehicle
Patent: US 6321716-A 531 27-NOV-2001;
Location/Qualifiers

879 bp DNA linear PAT 29-JAN-2003

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL FEATURES	ORIGIN
Unknown. Unclassified.	1 (bases 1 to 879)			
Unknown.	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.	Compositions and methods for the therapy and diagnosis of prostate cancer	US 6512094-A 531 28-JAN-2003; Location/Qualifiers 1. 879 /organism="unknown" /mol_type="genomic DNA"	
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Db	342	AAAGAGGACTGCTTACATCTGGGCTCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCGT	401	
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Qy	579	AAATATTCAGATGAGTATGAAATACACCTTACACTATGCTGTCTCAATGAAGATAA	638	
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Qy	819	TGTAATGTTGGATCAGCAAGATATAGTCAGCCCTCTACTTGGACAAATGTTGATGATC	878	
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QY	759	CAAGGAAATACGCAATTTAAATGCGCTGGATAGATATGGAGAACTGCTCTCATCTTGC	761
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DEFINITION Sequence 531 from patent US 6329505.
ACCESSION AR367286
VERSION AR367286.1 GI:34600261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 531 11-DEC-2001;
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Best Local Similarity 99.8%; Pred. No. 0;
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QY 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTCTGGAGACCACACGACCTCTGTGAA 158
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QY 879 TTCTCAAGATCTGAAAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGAAAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 4
AR400322
LOCUS AR400322 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 531 from patent US 6620922.
ACCESSION AR400322
VERSION AR400322.1 GI:40143587
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvik,T.S., Cartez,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 531 16-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTCTGGAGACCACACGACCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTCTGGAGACCACACGACCTCTGTGAA 101

QY 159 GACGCTTGGGAGCAAGAGTGCAAGTGGTGTGCTGCCACTGCTTCCCCTGCTGAGGGGAG 218
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QY 339 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGAGCAAGCA 398
Db 282 CCCAGAAAGGATCTCATGCTCAGGAGCACTGATGTGAACAAGAGGAGCAAGCA 341

QY 399 AAAGAGGAGTCTCATGCTCAGGAGCACTGATGTGAACAAGAGGAGCAAGCA 458
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Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCTCTTACCTTGGCAAAAGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCAATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCAATCATG 876

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LOCUS AR405589 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 531 from patent US 6630305.
ACCESSION AR405589
VERSION AR405589.1 GI:40154426
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Sheiky, Y.A.W., Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 531 07-OCT-2003;
FEATURES Location/Qualifiers
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Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 101
Qy 159 GACGCTTGGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
Qy 219 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCAATGATCCAG 278
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Qy 459 GCTGGACAGAGTGTCAACTTAATGCTCTTGAACAAACAAAGAGGACAGCTCTGACAAA 518
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Db 762 TGTATGTTGGATCAGCAAGTATAGTACGCTCTTACCTTGGCAAAAGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCAATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGCCAGAGATGATGCTGTTTCTAGTCAATCATG 876

RESULT 6
AR433323
LOCUS AR433323 879 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 314 from patent US 6656480.
ACCESSION AR433323
VERSION AR433323.1 GI:40196105
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 879)
AUTHORS Retter, M.W., and Dillon, D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6656480-A 314 02-DEC-2003;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 101
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Db 102 GACGCTTGGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
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Db 222 GTACCACTGATGGAAGATCTGGAACAGCTCCACAGAGCTGCTGGTGGGTAAGT 281
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Db |||||

RESULT 7
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LOCUS AX141041 879 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 531 from Patent WO0134802.
ACCESSION AX141041
VERSION AX141041.1 GI:14281098
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skeiky, Y.A. and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 531 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGCGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCTCTCTGTGAA 158
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QY 159 GACCTTTGGAGCAAGAGTGTGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGGAG 218
Db |||||
QY 219 CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGATCCAG 278
Db |||||
QY 279 GTACCACTCCATGGAAGAGATCTGGAACAAGCTCCACAGAGCTGCTGGGGTAAAGT 338
Db |||||
QY 339 CCCCAGAGAGATCTCATGCTCATGCTCAGGACACATGATGTAACAGAGGACAGCA 398
Db |||||
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QY 459 GCTGAGACAGAGTGTCAACTTANTGCTTGAACAAGAGAGGACAGCTCTGACAAA 518
Db |||||
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Db |||||
QY 759 CAGAAAAGAGCAATTTAAATGCGCTGATATGATGAGCACTGCTCATACTTGC 818
Db |||||
QY 819 TGTATGTTGGATCAGCAAGTATAGTACGCTTCTACTTGGACAAATGTTGATGATC 878
Db |||||

RESULT 8
AX200901
LOCUS AX200901 879 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 531 from Patent WO0151633.
ACCESSION AX200901
VERSION AX200901.1 GI:15390769
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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Qy      879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db      822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 10
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LOCUS      AX316977      879 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 314 from Patent WO0190152.
ACCESSION AX316977
VERSION    AX316977.1 GI:17900048
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
            Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE       Compositions and methods for the therapy and diagnosis of breast
            cancer
JOURNAL     Patent: WO 0190152-A 314 29-NOV-2001;
            CORIXA CORPORATION (US);
FEATURES    Location/Qualifiers
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ORIGIN
Query Match      78.6%; Score 733; DB 6; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
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Db      102 GACGCTTGGAGCAAGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
Qy      219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCCAG 278
Db      162 CGGCAAGAGCAACGTGGTCCCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCCAG 221
Qy      279 GTACCAAGTCCATGGAGAAAGTGGGCAAGCTCCACAGAGCTGCTGGTGGGTTAAAGT 338
Db      222 GTACCAAGTCCATGGAGAAAGTGGGCAAGCTCCACAGAGCTGCTGGTGGGTTAAAGT 281
Qy      339 CCCAGAAAGGATCTATCTGCTCAGGACACTGTATGTGAAACAGAGGACAGCA 398
Db      282 CCCAGAAAGGATCTATCTGCTCAGGACACTGTATGTGAAACAGAGGACAGCA 341
Qy      399 AAAGAGGACTGCTCTACATCTGGCTCTGCAATGGGAAATTCAGAAAGTAGTAAATCTGT 458
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Qy      459 GCTGGACAGAGGATGTCATCTTAATGTCCTTGACACAAAAAGAGGACAGCTCTGACAAA 518
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Qy      759 CAAGAAAAAAGCGAAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818
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Qy      819 TGTATGTTGGTGGATCAGCAAGTATAGTACGCTCTACTTGACCAAAATGTTGATGATTC 878
Db      762 TGTATGTTGGTGGATCAGCAAGTATAGTACGCTCTACTTGACCAAAATGTTGATGATTC 821
Qy      879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db      822 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 11
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LOCUS      AR261058      1852 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION Sequence 530 from patent US 6321716.
ACCESSION AR261058
VERSION    AR261058.1 GI:28071821
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1852)
AUTHORS     Mashiki,Z. and Harada,J.
TITLE       Negative pressure control apparatus for engine mounted in vehicle
JOURNAL     Patent: US 6321716-A 530 27-NOV-2001;
FEATURES    Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      99 CAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
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Qy      159 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db      831 GACGCTTGGAGCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 890
Qy      219 CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCCAG 278
Db      891 CGGCAAGAGCAACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 950
Qy      279 GTACCAAGTCCATGGAGAAAGTCTGGAACAGCTCCACAGAGCTGCTGGTGGGTTAAAGT 338
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QY	219	CGGCAAGAGCAACGCTGGCGCTTGGGGAGACTACGATGACAGCGGCTTTCATGATCCAG	278
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QY	279	GTACCACTCCATGGAGAGTCTGGCAAGCTTCCAGAGCTGCTGGTGGGGTAAAGT	338
DB	951	GTACCACTCCATGGAGAGTCTGGCAAGCTTCCAGAGCTGCTGGTGGGGTAAAGT	1010
QY	339	CCCCAGAAAGGATCTCATCGTCTCAGGAGCACTGATGTGAACAAGAGGGAACAAGCA	398
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QY	399	AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT	458
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QY	459	GCTGGACAGACGATGTCAACTTAATGTCTTGCACAAACAAAGAGGACAGCTCTGACAAA	518
DB	1131	GCTGGACAGACGATGTCAACTTAATGTCTTGCACAAACAAAGAGGACAGCTCTGACAAA	1190
QY	519	GGCCGTACAAATGCCAGGAGATGTAATGTCGTTAATGTTGCTGGAACATGGCACTGATCC	578
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QY	639	ATTAATGGCCAAAGCACTGCTCTTACGGTCTGATATCGAATCAAAAACAAAGCATGG	698
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DB	1371	CCTCACACCACTGCTACTTGGTATACATGACAAACAGCAAGTGGTGAATTTTAAAT	1430
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QY	879	TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCAATCATG 933	
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DEFINITION			
SEQUENCE 530 from patent US 6620922.			
ACCESSION			
AR400321			
VERSION			
AR400321.1 GI:40143584			
KEYWORDS			
Unknown.			
SOURCE			
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ORGANISM			
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AR400321 LOCUS 1852 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 530 from patent US 6620922.
ACCESSION AR400321
VERSION AR400321.1 GI:40143584
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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LOCUS AR405588 1852 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 530 from patent US 6630305.
ACCESSION AR405588
VERSION AR405588.1 GI:40154425
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1852)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fager, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Sheiky, Y.A.W.,
Hepler, W.T., and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 530 07-OCT-2003;
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACGTGGGCACCTTTGGAGACCAACAGACTCTCTGTGAA 158
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Qy 159 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCTCCCTGCTGCGAGGGGGAG 218
Db 831 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCTCCCTGCTGCGAGGGGGAG 890
Qy 219 CGGCAAGAGCAACGTGGGCGCTTTGGGAGACTACGATGACAGGCGCTTCATGGATCCCAG 278
Db 891 CGGCAAGAGCAACGTGGGCGCTTTGGGAGACTACGATGACAGGCGCTTCATGGATCCCAG 950
Qy 279 GTACAGCTCCATGAGAGATCTGGAGAGCTTGGAGAGCTCCAGAGCTGCTGGTGGGTTAAAGT 338
Db 951 GTACAGCTCCATGAGAGATCTGGAGAGCTTGGAGAGCTCCAGAGCTGCTGGTGGGTTAAAGT 1010
Qy 339 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGTGTGAACAAGAGGGACCAAGCA 398
Db 1011 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGTGTGAACAAGAGGGACCAAGCA 1070
Qy 399 AAGAGGACTGCTCTACATCTGGCTCTGCCATGGGAATTCAGAGTAGTAAACTCGT 458
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Qy 459 GCTGCAGACGAGTGTCAACTTAATGTCTTGACACAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGCAGACGAGTGTCAACTTAATGTCTTGACACAAAAGAGGACAGCTCTGACAAA 1190
Qy 519 GGCGGTACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACATGGCACTGATCC 578
Db 1191 GGCGGTACATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACATGGCACTGATCC 1250
Qy 579 AAATATTCAGATGAGTAAATACCACTACACTATGCTGTACAAATGAAGATAA 638
Db 1251 AAATATTCAGATGAGTAAATACCACTACACTATGCTGTACAAATGAAGATAA 1310
Qy 639 ATTAATGCCAAAGCACTGCTTTATAGGTTGCTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCCAAAGCACTGCTTTATAGGTTGCTGATATCGAATCAAAAAACAAGCATGG 1370
Qy 699 CCTCACACCACTGCTACTTGTATACATGACCAAAACAGCAAGTGGTGAATTTTAAAT 758
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SUMMARIES

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7	733	78.6	879	4	AAh93826 Human pro
8	733	78.6	879	4	AAh85140 Human pro
9	733	78.6	879	5	AAh59727 Prostate
10	733	78.6	879	6	AAh93825 Human pro
11	733	78.6	879	6	AAh93826 Human pro
12	733	78.6	879	7	AAc94454 Prostate
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14	733	78.6	879	9	Adc15366 Human bre
15	733	78.6	879	9	Adc15396 Human bre
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19	733	78.6	879	4	AAh85139 Human pro
20	733	78.6	879	4	AAh85139 Human pro
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ALIGNMENTS

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ID ADc15395 standard; DNA; 933 BP.
AC ADc15395;
DT 18-DEC-2003 (first entry)
XX Human breast tumour protein DNA, SEQ ID 343.
DE Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.
KW Homo sapiens.
XX WO2003013431-A2.
XX 20-FEB-2003.
XX 05-AUG-2002; 2002WO-US024917.
XX 07-AUG-2001; 2001US-00924400.
XX 20-FEB-2002; 2002US-00079137.
XX 02-AUG-2002; 2002US-00212679.
(CORI-) CORIXA CORP.
Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
Kalos MD;
WPI; 2003-342398/32.
New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.
Claim 1; SEQ ID NO 343; 308pp; English.

The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells

CC specific for the tumour protein. The present sequence was used to CC illustrate the invention.

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	Best Local Similarity	100.0%; Pred. No. 0;
	Matches	933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	361	ATGCTCAGGGACACTGATGTGAAACAAAGAGGACAAGCAAAAGAGGACTGCTCTACATCTG 420
Qy	421	GCCTCTGCAATGGGAATTCAGAGTAGTATAAACTGTGTGTGACAGACGATGCAACTT 480
Db	421	GCCTCTGCAATGGGAATTCAGAGTAGTATAAACTGTGTGTGACAGACGATGCAACTT 480
Qy	481	AATGTCCTTTGACAAACAAAAGAGACAGCTCTGCAAAAGGCCGTACAAATGCCAGGAAGAT 540
Db	481	AATGTCCTTTGACAAACAAAAGAGACAGCTCTGCAAAAGGCCGTACAAATGCCAGGAAGAT 540
Qy	541	GAATGTGCGTTAATGTTGCTGGAACTAGGCACACTGATCCAAATATTCACAGATGAGTATGGA 600
Db	541	GAATGTGCGTTAATGTTGCTGGAACTAGGCACACTGATCCAAATATTCACAGATGAGTATGGA 600
Qy	601	AATACCACTCTACACTATGCTGTCTACAATCAAGATAAAATTAATGGCCCAAGCACTGCTC 660
Db	601	AATACCACTCTACACTATGCTGTCTACAATCAAGATAAAATTAATGGCCCAAGCACTGCTC 660
Qy	661	TTATACGGTGTGATATCGAATCAAAAACCAAGCATGGCCCTCACACCACTGCTACTTGGT 720
Db	661	TTATACGGTGTGATATCGAATCAAAAACCAAGCATGGCCCTCACACCACTGCTACTTGGT 720
Qy	721	ATACATGAGCAAAAACCAAGCAAGTGGTGAATTTTTTAATCAAGAAAAAGCGAATTTAAAT 780
Db	721	ATACATGAGCAAAAACCAAGCAAGTGGTGAATTTTTTAATCAAGAAAAAGCGAATTTAAAT 780
Qy	781	CGCTGGATAGATATGGAAGAACTGCTCTCATCTTGTCTATGTTGTGGATCAGCAAGT 840
Db	781	CGCTGGATAGATATGGAAGAACTGCTCTCATCTTGTCTATGTTGTGGATCAGCAAGT 840
Qy	841	ATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAAGCGG 900
Db	841	ATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAAGCGG 900
Qy	901	CCAGAGAGTATGCTGTTTCTTAGTCATCATCATG 933
Db	901	CCAGAGAGTATGCTGTTTCTTAGTCATCATCATG 933

RESULT 2
ADCI5394
ID ADCI5394 standard; DNA; 876 BP.
XX
AC AC
ADCI5394;
XX
18-DEC-2003 (first entry)
DT
XX
Human breast tumour protein DNA, SEQ ID 342.
DE
XX
Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW ds.
KW
XX
Homo sapiens.
OS
XX
W02003013431-A2.
PN
XX
20-FEB-2003.
PD
XX
05-AUG-2002; 2002WO-US024917.
PP
XX
07-AUG-2001; 2001US-00924400.
PR
XX
20-FEB-2002; 2002US-00079137.
PR
XX
02-AUG-2002; 2002US-00212679.
PR
XX
(CORI-) CORIXA CORP.
PA
XX
Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
PI
XX
WPI; 2003-342398/32.
DR
XX
New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
PT
XX
Claim 1; SEQ ID NO 342; 308pp; English.
PS
XX
The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.

SQ	Sequence	876 BP;	261 A;	193 C;	222 G;	200 T;	0 U;	0 Other;	
	Query Match	89.5%;	Score 835;	DB 9;	Length 876;				
	Best Local Similarity	100.0%;	Pred. No. 0;						
	Matches 835;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	99	CAGGGGCGGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA	158						
DB	42	CAGGGGCGGGCAAGAGCAACGCTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA	101						
QY	159	GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCTGTGTCAGGGGGAG	218						
DB	102	GACGCTTGGGAGCAAGAGGTGCAAGTGGTGCTGCCACTGCTTCCCTGTGTCAGGGGGAG	161						
QY	219	CGSCAAGAGCAACGCTGGGCGCTTTGGGGAGACTACGATGACAGCGCCTTCATGATCCAG	278						
DB	162	CGSCAAGAGCAACGCTGGGCGCTTTGGGGAGACTACGATGACAGCGCCTTCATGATCCAG	221						
QY	279	GTACCAAGCTCCATGGAGAGATCTGGCAAGCTTCCACAGAGCTGCTGGTGGGGTAAAGT	338						
DB	222	GTACCAAGCTCCATGGAGAGATCTGGCAAGCTTCCACAGAGCTGCTGGTGGGGTAAAGT	281						
QY	339	CCCAGAAAGGATCTCATGCTCATGCTCAGGGGACACTGATGTAAACAAGAGGGACAAAGCA	398						

Db 282 CCCAGAAAGGATCTCATCTGCTCAGGACACTGATGTGACAAAGGAGGACAGCA 341
Qy 399 AAAGAGGACTCTCTACATCTGGGCTCTGCAATGGGAATTCAGAGTAGTAAACTCGT 458
Db 342 AAAGAGGACTCTCTACATCTGGGCTCTGCAATGGGAATTCAGAGTAGTAAACTCGT 401
Qy 459 GCTGACAGAGATGTCAACTTAATGCTTGTGACACAAAGGAGGACAGCTCTGACAA 518
Db 402 GCTGACAGAGATGTCAACTTAATGCTTGTGACACAAAGGAGGACAGCTCTGACAA 461
Qy 519 GGCGTCAATGCCAGGAGATGAATGCGTTAATGTTGCGAAACATGCCATGATCC 578
Db 462 GGCGTCAATGCCAGGAGATGAATGCGTTAATGTTGCGAAACATGCCATGATCC 521
Qy 579 AAATATCCAGATGATGAAATACACCTCTACACTATGCTCTCTACATGAGATA 638
Db 522 AAATATCCAGATGATGAAATACACCTCTACACTATGCTCTCTACATGAGATA 581
Qy 639 ATTAATGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAGCATGG 641
Qy 699 CTTACACACTCTCTATGTTGATACATGACCAAAACAGCAAGTGTGAAATTTTAAT 758
Db 642 CTTACACACTCTCTATGTTGATACATGACCAAAACAGCAAGTGTGAAATTTTAAT 701
Qy 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATCTTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATCTTGC 761
Qy 819 TGTATGTTGTGGATCAGCAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGGATCAGCAATATAGTCAGCCCTCTACTTGAGCAAAATGTTGATGATC 821
Qy 879 TTCTCAAGATCTGGAAGACGCGCAGAGATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGCGCAGAGATGCTGTTTCTAGTCATCATG 876

RESULT 3
ADCL5396 standard; DNA; 939 BP.
XX ADCL5396;
XX
DT 18-DEC-2003 (first entry)
DE Human breast tumour protein DNA, SEQ ID 344.
XX
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.
XX
XX Homo sapiens.
XX
PV WO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
XX 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
XX (CORI-) CORIYA CORP.
XX
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
XX WPI; 2003-342398/32.
XX
XX New polynucleotide, useful for preparing a composition for diagnosing,

PT treating or preventing cancer.
XX Claim 1; SEQ ID NO 344; 309pp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.

XX Sequence 939 BP; 273 A; 204 C; 249 G; 213 T; 0 U; 0 Other;

Query Match 80.2%; Score 748; DB 9; Length 939;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 848; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 84 CTGCTTTCCCTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAA 143
Db 90 CTGCTTTCCCTGCTCAGGGGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACAA 149
Qy 144 CGACTCTCTGTGAAGACGCTTTGGGAGCAAGAGGTGCAAGTGGTGGTGGTGGTGGT 203
Db 150 CGACTCTCTGTGAAGACGCTTTGGGAGCAAGAGGTGCAAGTGGTGGTGGTGGTGGT 209
Qy 204 CTGCTGCAAGGGGAGCGGCAAGAGCAACGTGGGCGCTTGGGAGACTAGATGACAGCGC 263
Db 210 CTGCTGCAAGGGGAGCGGCAAGAGCAACGTGGTGGTGGGAGACTAGATGACAGCGC 269
Qy 264 CTTCTAGGATCCCAAGTACCACTGATGAGCAAGATCTGGCAAGCTCCACAGAGCTGC 323
Db 270 CTTCTAGGATCCCAAGTACCACTGATGAGCAAGATCTGGCAAGCTCCACAGAGCTGC 329
Qy 324 CTGCTGGGTTAAAGTCCCAAGAGATCTCATCTGCTCAGGACACTGATGTGAA 383
Db 330 CTGCTGGGTTAAAGTCCCAAGAGATCTCATCTGCTCAGGACACAGGATGTGAA 389
Qy 384 CAAGAGGCAACAGCAAGAGAGGACTGCTCATCTGGGCTCTGCCAATGGGAATTCAGA 443
Db 390 CAAGAGGCAACAGCAAGAGAGGACTGCTCATCTGGGCTCTGCCAATGGGAATTCAGA 449
Qy 444 AGTAGTAAACTCGTCTGACAGAGATGTCAACTTAATGTCCTTGAACAACAAAGAG 503
Db 450 AGTAGTAAACTCGTCTGACAGAGATGTCAACTTAATGTCCTTGAACAACAAAGAG 509
Qy 504 GACAGCTCTGACAAAGCGGCTACATGCCAGAGATGAATGTCGTTAATGTTGCTGGA 563
Db 510 GACAGCTCTGACAAAGCGGCTACATGCCAGAGATGAATGTCGTTAATGTTGCTGGA 569
Qy 564 ACATGGCACTGATCCAAATATTTCCAGATGAGTATGGAATACCACTCTACATGCTGT 623
Db 570 ACATGGCACTGATCCAAATATTTCCAGATGAGTATGGAATACCACTCTACATGCTGT 629
Qy 624 CTRCAATGAGATAAATTAATGCGCAAGCACTGCTCTTATACGGTGGTGTATCGAATC 683
Db 630 CTACAATGAGATAAATTAATGCGCAAGCACTGCTCTTATACGGTGGTGTATCGAATC 689
Qy 684 AAAAAACAAGCATGGGCTCACACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGT 743
Db 690 AAAAAACAAGCATGGGCTCACACCACTGCTACTTGTATACATGAGCAAAAAACAGCAAGT 749
Qy 744 GGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAC 803
Db 750 GGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAC 809
Qy 804 TGTCTCTACTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
Db 810 TGTCTCTACTTGTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 869

QY 864 AAATGTTGATGATCTTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTCTAGT 923
DB |||||
870 AAATGTTGATGATCTTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTCTAGT 929
QY 924 CATCATCATG 933
DB |||||
930 CATCATCATG 939

RESULT 4
ADCL5393
ID ADC15393 standard; DNA; 876 BP.
XX
AC ADC15393;
XX
18-DEC-2003 (first entry)
XX
DE Human breast tumour protein DNA, SEQ ID 341.
XX
KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KW ds.
XX
OS Homo sapiens.
XX
PN W02003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR WPI; 2003-342398/32.
XX
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
XX
PS Claim 1; SEQ ID NO 341; 308pp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which simulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 876 BP; 261 A; 193 C; 222 G; 200 T; 0 U; 0 Other;

Query Match 78.8%; Score 733; DB 9; Length 876;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGGAGCGGCAAGACCAACCTGGGCGACTCTTGAGACCAACAGACTCTCTGTGAA 158
DB |||||
42 CAGGGGGAGCGGCAAGACCAACCTGGGCGACTCTTGAGACCAACAGACTCTCTGTGAA 101
QY 159 GAGCCTTGGAGCAAGAGGTGCAAGTGTGCTGCCACTGCTCCCTGCTGCAGGGGAG 218
DB |||||
102 GAGCCTTGGAGCAAGAGGTGCAAGTGTGCTGCCACTGCTCCCTGCTGCAGGGGAG 161

QY 219 CGGCAAGAGCAACGTGGGCGCTTGGGAGAGTACGATGACAGGCGCCCTTCATGGATCCAG 278
DB |||||
162 CGGCAAGAGCAACGTGGTCTGCTTGGGAGAGTACGATGACAGGCGCCCTTCATGGATCCAG 221
QY 279 GTACACGTCCTCCTGGAAGATCTGGAAGAGTCCAGAGCTCCAGAGCTGCTGGTGGGTAAGT 338
DB |||||
222 GTACACGTCCTCCTGGAAGATCTGGAAGAGTCCAGAGCTCCAGAGCTGCTGGTGGGTAAGT 281
QY 339 CCCAGAAAGGATCTCATGCTGATGCTCAGGAGCACCTGATGTGAACAGAGGGAACAAGCA 398
DB |||||
282 CCCAGAAAGGATCTCATGCTGATGCTCAGGAGCACCGGATGTGAACAGAGGGAACAAGCA 341
QY 399 AAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAGTAGTAAACTCGT 458
DB |||||
342 AAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAGTAGTAAACTCGT 401
QY 459 GCTGGACAGAGTGTCAACTTAAATGCTCTGACCAACAAAGAGGAGGACGCTCTGACAAA 518
DB |||||
402 GCTGGACAGAGTGTCAACTTAAATGCTCTGACCAACAAAGAGGAGGACGCTCTGACAAA 461
QY 519 GGCGGTACAATGCCAGGAAGATGTAATGCGTTAAATGCTGGAACATGGCACTGATCC 578
DB |||||
462 GGCGGTACAATGCCAGGAAGATGTAATGCGTTAAATGCTGGAACATGGCACTGATCC 521
QY 579 AATATTCCAGATGAGTATGGAATACCACTCTACACTATGCTGTACAAATGAAGATAA 638
DB |||||
522 AATATTCCAGATGAGTATGGAATACCACTCTACACTATGCTGTACAAATGAAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAAGCATGG 698
DB |||||
582 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTCTGATACATGACCAACCAACAGCAAGTGTGAAATTTTAAAT 758
DB |||||
642 CCTCACACCACTGCTCTGATACATGACCAACCAACAGCAAGTGTGAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATCGAATCAAAAACAAGCATGG 818
DB |||||
702 CAAGAAAAAGCGAATTTAAATGCGTGTGATATCGAATCAAAAACAAGCATGG 761
QY 819 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCMAAATGTTGATGTATC 878
DB |||||
762 TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTACTTTGAGCMAAATGTTGATGTATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
DB |||||
822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 5
AAC81016
ID AAC81016 standard; cDNA; 879 BP.
XX
AC AAC81016;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human breast tumour-specific antigen cDNA SEQ ID NO: 314.
XX
KW Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
OS Homo sapiens.
XX
PN W0200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US009312.
XX
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.

XX (CORI-) CORIXA CORP.
XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX WPI: 2000-628403/60.
XX P-FSDb; AAB28636.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
XX tumor protein used for inhibiting the development of cancer, especially
XX breast cancer, and monitoring cancer progression in a patient.
XX
XX Claim 4; Page 185-186; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
XX and methods for the treatment and diagnosis of breast cancer. Nucleotide
XX sequences that are preferentially expressed in breast tumour tissue, and
XX the polypeptides encoded by such nucleotide sequences, are used in
XX compositions and vaccines to inhibit the development of cancer,
XX especially breast cancer. The progression of a cancer may be monitored by
XX carrying out detection of tumour-specific antigens at subsequent time
XX points and comparing the results from the different time points. CD4+
XX and/or CD8+ T-cells isolated from the cancer patient may be treated with
XX tumour-specific polypeptides, polynucleotides encoding the polypeptides
XX or antigen presenting cells expressing the polypeptides. The cells are
XX then administered to the patient to inhibit development of cancer
XX
XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
XX
XX Query Match 78.6%; Score 733; DB 3; Length 879;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 99 CAGGGGAGGGGCAAGAGCAACGCTGGGCACTTCTGGAGACACAAACGACTCCTCTGTGAA 158
XX
XX 42 CAGGGGAGGGGCAAGAGCAACGCTGGGCACTTCTGGAGACACAAACGACTCCTCTGTGAA 101
XX
XX 159 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTCTGCTGCACTGCTCCCTCTGGAGGGGGAG 218
XX
XX 102 GACGCTTTGGGAGCAAGAGGTGCAAGTGGTCTGCTGCACTGCTCCCTCTGGAGGGGGAG 161
XX
XX 219 CGGCAAGAGCAACGCTGGGCGCTGGGAGACTAGATGACAGCGCTTCAATGGATCCAG 278
XX
XX 162 CGGCAAGAGCAACGCTGGGCGCTGGGAGACTAGATGACAGCGCTTCAATGGATCCAG 221
XX
XX 279 GTACACGCTCCATGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGGGTAAAGT 338
XX
XX 222 GTACACGCTCCATGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGGGTAAAGT 281
XX
XX 339 CCCAGAAAGGATCTCATCTGCTCAGGGACACTGTGTGAACAAGAGGGACAAAGCA 398
XX
XX 282 CCCAGAAAGGATCTCATCTGCTCAGGGACAGGGATGTGAACAAGAGGGACAAAGCA 341
XX
XX 399 AAAGAGAGCTGCTTACATCTGGCTTGGCAATGGGAATTCAGAGTAGTAAACTCGT 458
XX
XX 342 AAAGAGAGCTGCTTACATCTGGCTTGGCAATGGGAATTCAGAGTAGTAAACTCGT 401
XX
XX 459 GCTGGACAGAGCTGCTCAACTTAATGCTTGAACAACAAGAGGACAGCTCTGCAAA 518
XX
XX 402 GCTGGACAGAGCTGCTCAACTTAATGCTTGAACAACAAGAGGACAGCTCTGCAAA 461
XX
XX 519 GGCGGTACATGGCAGGAAGATGATGGTAAATGTTCTGGACATGGCACTGATCC 578
XX
XX 462 GGCGGTACATGGCAGGAAGATGATGGTAAATGTTCTGGACATGGCACTGATCC 521
XX
XX 579 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTACAGTAAAGATAA 638
XX
XX 522 AATATTTCCAGATGAGTATGGAATACCACTTACACTATGCTGTACAGTAAAGATAA 581
XX
XX 639 ATTAATGCCAAGCACTGCTTTATACGCTGTGATATCGAATCAAAAACAAGCATGG 698
XX
XX 582 ATTAATGCCAAGCACTGCTTTATACGCTGTGATATCGAATCAAAAACAAGCATGG 641

QY 699 CCTCACCACTGCTACTTGGTATATCATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGGTATATCATGAGCAAAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATACTTGC 761
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAAGCCCTCTACTTGGAGCAAAATGTTGATGTATC 878
Db 762 TGTATGTTGTGATCAGCAAGTATAGTCAAGCCCTCTACTTGGAGCAAAATGTTGATGTATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGATGCTGTTTCTAGTCATCATCATG 876
RESULT 6
AAH93826
ID AAH93826 standard; cDNA; 879 BP.
XX
XX AAH93826;
AC
XX 04-OCT-2001 (first entry)
DT
XX Human prostate-specific cDNA sequence splice variant open reading frame.
DE
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW
XX cytostatic; gene therapy; metastasis; ss.
KW
XX Homo sapiens.
OS
XX WO200151633-A2.
PN
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001WO-US001574.
PF
XX 14-JAN-2000; 2000US-00483672.
PR
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
PI
XX WPI: 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
PT
XX Claim 1; Page 408; 543pp; English.
PS
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
XX Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
SQ
XX Query Match 78.6%; Score 733; DB 4; Length 879;
XX Best Local Similarity 99.8%; Pred. No. 0;

[illegible]

PN	WO200173032-A2.
XX	
PD	04-OCT-2001.
XX	
PX	27-MAR-2001; 2001WO-US009919.
PF	
XX	
PR	27-MAR-2000; 2000US-0036857.
PR	09-MAY-2000; 2000US-00568100.
PR	12-MAY-2000; 2000US-00570737.
PR	13-JUN-2000; 2000US-00593793.
PR	27-JUN-2000; 2000US-00605783.
PR	09-AUG-2000; 2000US-00636215.
PR	29-AUG-2000; 2000US-00651236.
PR	06-SEP-2000; 2000US-006572729.
PR	02-OCT-2000; 2000US-00679420.
PR	10-OCT-2000; 2000US-00685166.
PR	09-NOV-2000; 2000US-00709729.
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Ratter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX	
DR	WPI: 2001-639232/73.
DR	P-PSTB; AU69821.
XX	
XX	New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.
PT	
PT	Claim 1; Page 408; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention
XX	
SQ	Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;
Query Match	78.6%; Score 733; DB 4; Length 879;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 833; Conservative	0; Mismatches 2; Indels 0; Gaps 0
QY	99 CAGGGGAGCGCAGACAGCAACGTGGGCATCTTCGGAGACCACAACACTCCTCTGTGAA 158
Db	42 CAGGGGAGCGCAGACAGCAACGTGGGCATCTTCGGAGACCACAACACTCCTCTGTGAA 101
QY	159 GACGTTTGGAGCAAGAGGTCAAAGTGCTGCCACTGCTTCCCCTGTGACGGGGAG 218
Db	102 GACGTTTGGAGCAAGAGGTCAAAGTGCTGCCACTGCTTCCCCTGTGACGGGGAG 161
QY	219 CGCGAAGAGCAACGTGGCGCTTCGGGAGACTAGATGACAGCGCTTCATGATCCCAG 278
Db	162 CGCGAAGAGCAACGTGGCTTCGGGAGACTAGATGACAGCGCTTCATGATCCCAG 221
QY	279 GTACCACTCCATGAGAAGATCTGGAACAGCTCCACAGAGCTGCCTGTGGGGTAAGT 338
Db	222 GTACCACTCCATGAGAAGATCTGGAACAGCTCCACAGAGCTGCCTGTGGGGTAAGT 281
QY	339 CCCCGAAGAGTCTCATCGTCATGCTCAGGGACACTGATGTGAACAAGGGGACAAGCA 398
Db	282 CCCCGAAGAGTCTCATCGTCATGCTCAGGGACACGGATGTGAACAAGGGGACAAGCA 341
QY	399 AAAGAGGACTGCTTACATCTGGCCTCTGCCAATGGGAATTCAAGTAGTATAAACTCGT 458

Db 342 AAGAGGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 401
QY 459 GCTGACACAGCATGTCAACTTAATGTCTTTGACACAAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGACACAGCATGTCAACTTAATGTCTTTGACACAAAAGAGGACAGCTCTGACAAA 461
QY 519 GGCCTATCAATGCCAGGAAGATGAATGCGCTTAATGTCTTGTGGAACATGGCACTGATCC 578
Db 462 GGCCTATCAATGCCAGGAAGATGAATGCGCTTAATGTCTTGTGGAACATGGCACTGATCC 521
QY 579 AAATATTCCAGATGAGTAAATACCACTCTACACTATGCTCTCTACAATGAAGATAA 638
Db 522 AAATATTCCAGATGAGTAAATACCACTCTACACTATGCTCTCTACAATGAAGATAA 581
QY 639 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCATGG 698
Db 582 ATTAATGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAACAGCATGG 641
QY 699 CCTCACCACTGCTACTTGTGTATACATGACGCAAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 642 CCTCACCACTGCTACTTGTGTATACATGACGCAAAAACAGCAAGTGGTGAATTTTAAAT 701
QY 759 CAAGAAAACCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 818
Db 702 CAAGAAAACCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATATTCG 761
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGTGACAAAATGTTGATGATC 878
Db 762 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGTGACAAAATGTTGATGATC 821
QY 879 TTCTCAAGATCTGAAAGACGCGCAGAGATGATGCTGTTTCTAGTCATCATCATG 933
Db 822 TTCTCAAGATCTGAAAGACGCGCAGAGATGATGCTGTTTCTAGTCATCATCATG 876

RESULT 8

AAH85140

ID AAH85140 standard; cDNA; 879 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

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XX AC

XX AC

Human prostate-specific sequence related cDNA sequence.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US030904.

12-NOV-1999; 99US-00439313.

18-NOV-1999; 99US-00443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Kalos MD, Retter MW, Stoik JA, Day CH, Skeiky YAW, Wang A;

WPI; 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, useful in the diagnosis and therapy of prostate cancer.

Claim 5; Page 308; 325pp; English.

Db 822 TTCTCAGATCTGGAAGACGGCCAGAGAGTATGCTGTTCTTAGTCATCATCATG 876

RESULT 9

ACA59727

XX ID ACA59727 standard; cDNA; 879 BP.

XX AC ACA59727;

XX DT 10-JUN-2003 (first entry)

XX DE Prostate cancer therapy associated cDNA #464.

XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW Prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.

XX OS Homo sapiens.

XX PN US2002192763-A1.

XX PD 19-DEC-2002.

XX PF 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

XX PR 04-OCT-2000; 2000US-00679272.

XX PR 28-MAR-2001; 2001US-00822827.

XX PA (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.

PA (MCNE/) MCNEILL P D.

PA (HOUG/) HOUGHTON R L.

PA (DRAS/) Y DE BASSOLS C V.

PA (FOYT/) FOY T M.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA,

PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX WPI; 2001-245062/25.

Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.

Example 11; SEQ ID NO 531; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 5; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACACGACTCTCTGTGAA 158
DB 42 CAGGGGGAGCGGCAAGAGCAAGCTGGGCACTTCTGGAGACCACACGACTCTCTGTGAA 101
QY 159 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTGCTTCCCTGCTGAGGGGAG 218
DB 102 GACGCTTGGGAGCAAGAGGTGCAAGTGGTGTGCTGCCACTGCTTCCCTGCTGAGGGGAG 161
QY 219 CGGCAAGAGCAAGCTGGGCGCTTGGGAGACTACGATCAGCGGCTTTCATGGATCCAG 278
DB 162 CGGCAAGAGCAAGCTGGTGGTGGGAGACTACGATCAGCGGCTTTCATGGATCCAG 221
QY 279 GTACCACGTCCATGGAGAGATCTGGACAAGTCCACAGAGCTGCTGGTGGGTAAGT 338
DB 222 GTACCACGTCCATGGAGAGATCTGGACAAGTCCACAGAGCTGCTGGTGGGTAAGT 281
QY 339 CCCGAGAAAGGATCTCATGCTCAGGACACTGATGTGAACAAGAGGGACAAGCA 398
DB 282 CCCGAGAAAGGATCTCATGCTCAGGACACTGATGTGAACAAGAGGGACAAGCA 341
QY 399 AAGAGGACTGCTTACATCTGGCTGCTGCCAATGGGAATTCAGAGTAGTAACCTG 458
DB 342 AAGAGGACTGCTTACATCTGGCTGCTGCCAATGGGAATTCAGAGTAGTAACCTG 401
QY 459 GCTGCACAGACGATGTCACCTTAATGTCTTGACAAACAAAGAGGACAGCTCTCACAAA 518
DB 402 GCTGCACAGACGATGTCACCTTAATGTCTTGACAAACAAAGAGGACAGCTCTCACAAA 461
QY 519 GGCCTGACATGCCAGGAGATGAATGGTGTGCTGGAACAATGCACTGATCC 578
DB 462 GGCCTGACATGCCAGGAGATGAATGGTGTGCTGGAACAATGCACTGATCC 521
QY 579 AATATTCAGATGATGGAATPACCACTCTACACTATGCTGTCTACAATGAAGATA 638
DB 522 AATATTCAGATGATGGAATPACCACTCTACACTATGCTGTCTACAATGAAGATA 581
QY 639 ATTATGGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
DB 582 ATTATGGCCAAAGCACTGCTTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTACTTGGTATACAGCAAAAAACAGCAAGTGGTAATTTTAAAT 758
DB 642 CCTCACCACTGCTACTTGGTATACAGCAAAAAACAGCAAGTGGTAATTTTAAAT 701
QY 759 CAAGAAAAAAGCAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACCTTC 818
DB 702 CAAGAAAAAAGCAATTTAAATGGCTGGATAGATATGGAAGAACTGCTCTCATACCTTC 761
QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTTCAGCAAAATGTTGATATC 878
DB 762 TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTTCAGCAAAATGTTGATATC 821
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
DB 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 876

RESULT 10

ABL95290

ID ABL95290 standard; cDNA; 879 BP.

XX

XX Example 11; Page 475; 691pp; English.

PS The present invention relates to novel prostate-specific proteins (PSP)

CC and their coding sequences. The PSPs and their coding sequences are

CC useful for stimulating an immune response in a patient, or for treating

CC prostate cancer in a patient and for determining, detecting or diagnosing

CC the presence of a cancer in a patient. The present sequence was used to

CC illustrate the invention

XX SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 7; Length 879;

Best Local Similarity 99.8%; Fred. No. 0;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGAGAGAGCAACGCTGGGCACTTCGGAGACCAACGACTCCTCTGTGAA 158

Db |||

QY 159 GACGTTGGGAGCAAGAGGTGAAGTGTGTGCTGCCACTGCTTCCCTGCTCGAGGGGAG 218

Db |||

QY 102 GACGTTGGGAGCAAGAGGTGAAGTGTGTGCTGCCACTGCTTCCCTGCTCGAGGGGAG 161

QY 219 CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 278

Db |||

QY 162 CGGCAAGAGCAACGCTGGGCGCTTGGGAGACTACGATGACAGCGCTTCATGGATCCAG 221

QY 279 GPACACGTCATGAGAGAGTCTGGACAAGCTCCACAGCTGCTGGTGGGTAAAGT 338

Db |||

QY 222 GPACACGTCATGAGAGAGTCTGGACAAGCTCCACAGCTGCTGGTGGGTAAAGT 281

QY 339 CCCAGAGAGGATCTCATGCTCATGCTCAGGACACGATGATGACAGAGGGGACAGCA 398

Db |||

QY 282 CCCAGAGAGGATCTCATGCTCATGCTCAGGACACGATGATGACAGAGGGGACAGCA 341

QY 399 AAAGAGGAGTCTCTACACTCTGGCTCTGCAATGGGAATTCAGAAAGTAGTAAACTCGT 458

Db |||

QY 342 AAAGAGGAGTCTCTACACTCTGGCTCTGCAATGGGAATTCAGAAAGTAGTAAACTCGT 401

QY 459 GCTGACAGACGATGTCAACTTAATGTCTCTGCAACAAAAGAGGACAGCTTGACAAA 518

Db |||

QY 402 GCTGACAGACGATGTCAACTTAATGTCTCTGCAACAAAAGAGGACAGCTTGACAAA 461

QY 519 GSCCGTACATGCCAGGAGATGAATGTGCTTAAATGTGCTGGAACATGCACTGATCC 578

Db |||

QY 462 GSCCGTACATGCCAGGAGATGAATGTGCTTAAATGTGCTGGAACATGCACTGATCC 521

QY 579 AAATATCCAGATGATGGAATACCACTCTACACTATGCTGTCTACAAATGAAGTAA 638

Db |||

QY 522 AAATATCCAGATGATGGAATACCACTCTACACTATGCTGTCTACAAATGAAGTAA 581

QY 639 ATTAATGCCAAGCACTGCTCTTATACGCTGATATCGATATCGAATCAAAAACAGCATGG 698

Db |||

QY 582 ATTAATGCCAAGCACTGCTCTTATACGCTGATATCGAATCAAAAACAGCATGG 641

QY 699 CUTCACACCTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 758

Db |||

QY 642 CUTCACACCTGCTACTTGGTATACATGAGCAAAAACAGCAAGTGGTGAATTTTAAAT 701

QY 759 CAAGAAAAGCGAATTAATGCGCTGGATAGATATGGAAGTCTCTCACTATGTC 818

Db |||

QY 702 CAAGAAAAGCGAATTAATGCGCTGGATAGATATGGAAGTCTCTCACTATGTC 761

QY 819 TGTATGTTGTGATCAGCAAGTATAGTCAGGCTCTACTTGGCAAAAATGTTGATGATC 878

Db |||

QY 762 TGTATGTTGTGATCAGCAAGTATAGTCAGGCTCTACTTGGCAAAAATGTTGATGATC 821

QY 879 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTTTCTAGTCATCATG 933

Db |||

QY 822 TTCTCAAGATCTGGAAGCGCCAGAGATATGCTTTCTAGTCATCATG 876

RESULT 13

ADAL1393

ID ADAL1393 standard; cDNA; 879 BP.

XX AC ADAL1393;

XX AC ADAL1393;

DT 06-NOV-2003 (first entry)

XX DE Human breast cancer specific full length cDNA B305D-A ORF.

XX ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.

XX Homo sapiens.

XX US2002165371-A1.

XX 07-NOV-2002.

XX 07-AUG-2001; 2001US-00924400.

XX 11-JAN-1996; 96US-00585392.

PR 10-JAN-1997; 97WO-US000485.

PR 09-APR-1997; 97US-00838762.

PR 11-DEC-1997; 97US-00991789.

PR 17-APR-1998; 98US-00062451.

PR 09-APR-1999; 99US-00289198.

PR 28-OCT-1999; 99US-00423755.

PR 23-MAR-2000; 2000US-00534825.

PR 24-MAY-2000; 2000US-00577505.

PR 08-JUN-2000; 2000US-00590583.

PR 26-OCT-2000; 2000US-00699295.

PR 16-MAR-2001; 2001US-00810936.

XX (FRUD/) FRUDAKIS T N.

PA (REED/) REED S G.

PA (SMIT/) SMITH J M.

PA (MISH/) MISHNER L E.

PA (DILL/) DILLON D C.

PA (RETT/) RETTER M W.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HARL/) HARLOCKER S L.

PA (DAYC/) DAY C H.

PA (LISX/) LI S X.

PA (DENG/) DENG T.

XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;

PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;

XX WPI: 2003-247262/24.

DR P-PSDB; ADAL1394.

XX New breast tumor proteins nucleic acids encoding such proteins, useful in

PT diagnosing, preventing and/or treating diseases such as cancer,

PT particularly breast cancer, and as markers for detecting the presence of

PT a cancer.

XX Claim 1; Page 149; 190pp; English.

XX The invention relates to a breast tumour polynucleotide selected from one

CC of the 275 fully defined nucleotide sequences (a) given in the

CC specification, including their complements in (a), sequences consisting of at

CC least 20 contiguous residues of a sequence in (a), sequences that

CC hybridise to a sequence in (a) under moderately stringent conditions,

CC sequences having at least 75% or 90% identity to a sequence in (a), or

CC degenerate variants of a sequence in (a). Also included are an isolated

CC polypeptide (II) comprising an amino acid sequence selected from

CC sequences encoded by (a), sequences having at least 70% or 90% identity

CC to a sequence encoded by (a), sequences of 30 fully defined amino acid

CC sequences (c), and sequences having at least 70% or 90% identity to a

CC sequence in (c), expression vectors comprising (a), a host cell

CC transformed or transfected with the expression vector, an isolated

CC antibody or its antigen-binding fragment that specifically binds to (II),

a method for detecting the presence of a cancer in a patient, a fusion protein comprising at least one polypeptide (II), an oligonucleotide that hybridises to (a), under moderately stringent conditions, a method for stimulating and/or expanding T cells specific for a tumour protein (by contacting T cells with at least one component selected from (a), (II) and antigen-presenting cells that express (II)), an isolated T cell population comprising T cells prepared from as detailed above, a method for stimulating an immune response or treating cancer in a patient by administering a composition comprising (a), (II), the vector, cells or the antibodies, and a method for inhibiting the development of a cancer in a patient. The polynucleotides may be used in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells. The breast tumour proteins are useful as markers to indicate the presence or absence of a cancer, such as breast cancer, and in the detection of other cancers. Compositions comprising the breast tumour proteins are useful in diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer. The present sequence is a breast cancer specific cDNA of the invention.

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 7; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	158
DB	42	CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	101
QY	159	GACGCTTGGGAGCAAGAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	218
DB	102	GACGCTTGGGAGCAAGAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	161
QY	219	CGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	278
DB	162	CGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	221
QY	279	GTACCACTCCATGAGAGATCTGGAGACACAAACACTCTCTGTGAA	338
DB	222	GTACCACTCCATGAGAGATCTGGAGACACAAACACTCTCTGTGAA	281
QY	339	CCCAGAGAGATCTCATCTGCTGCTGAGAGACACAAACACTCTCTGTGAA	398
DB	282	CCCAGAGAGATCTCATCTGCTGCTGAGAGACACAAACACTCTCTGTGAA	341
QY	399	AAAGAGGAGCTCTTACATCTGGGCTCTGCAATGGGAATTCAGAGTAACTCGT	458
DB	342	AAAGAGGAGCTCTTACATCTGGGCTCTGCAATGGGAATTCAGAGTAACTCGT	401
QY	459	GCTGACAGAGATGTCATCTTAATGCTTGGAGACACAAACACTCTCTGTGAA	518
DB	402	GCTGACAGAGATGTCATCTTAATGCTTGGAGACACAAACACTCTCTGTGAA	461
QY	519	GGCGGTACAAATCCAGGAGAGATGAATGCTGCTTAATGCTGGAACATGCACTATCC	578
DB	462	GGCGGTACAAATCCAGGAGAGATGAATGCTGCTTAATGCTGGAACATGCACTATCC	521
QY	579	AAATATCCAGATGAGTAAATACACTCTTACATCTGCTTCTTACATGAGATAA	638
DB	522	AAATATCCAGATGAGTAAATACACTCTTACATCTGCTTCTTACATGAGATAA	581
QY	639	ATTAATGCCAAGCACTGCTTATAGCGTCTGATATGAAATCAAAACAGCAATGG	698
DB	582	ATTAATGCCAAGCACTGCTTATAGCGTCTGATATGAAATCAAAACAGCAATGG	641
QY	699	CCTCACCACTGCTTATAGCGTCTGATATGAAATCAAAACAGCAATGG	758
DB	642	CCTCACCACTGCTTATAGCGTCTGATATGAAATCAAAACAGCAATGG	701
QY	759	CAAGAAAAGCGAATTTAAATGGCTGATATGAGAGTCTCTCTACTTTC	818
DB	702	CAAGAAAAGCGAATTTAAATGGCTGATATGAGAGTCTCTCTACTTTC	761

QY	819	TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTTCTTCTGAGCAAAATGTTGATATC	878
DB	762	TGTATGTTGGATCAGCAAGTATAGTCAGCCCTCTTCTTCTGAGCAAAATGTTGATATC	821
QY	879	TTCTCAAGATCTGGAAAGACCGCCAGAGATATGCTGTTTCTAGTCATCATCATG	933
DB	822	TTCTCAAGATCTGGAAAGACCGCCAGAGATATGCTGTTTCTAGTCATCATCATG	876

RESULT 14

ADCI5366
ID ADCI5366 standard; DNA; 879 BP.
XX
AC ADCI5366;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human breast tumour protein DNA, SEQ ID 314.
XX
XX Cytostatic; Gene therapy; breast cancer; breast tumour protein; human; ds.
XX Homo sapiens.
XX WO2003013431-A2.
XX 20-FEB-2003.
XX 05-AUG-2002; 2002WO-US024917.
XX 07-AUG-2001; 2001US-00924400.
XX 20-FEB-2002; 2002US-00079137.
XX 02-AUG-2002; 2002US-00212679.
XX (CORI-) CORIXA CORP.
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX WPI; 2003-342398/32.
XX New polynucleotide, useful for preparing a composition for diagnosing, treating or preventing cancer.
XX Example 1; SEQ ID NO 314; 308pp; English.

The present invention relates to compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer. The method for detecting the presence of a cancer in a patient comprises: obtaining a biological sample from the patient; contacting the biological sample with a binding agent that binds to the polypeptide; detecting in the sample an amount of the polypeptide that binds to the binding agent; and comparing the amount of the polypeptide to a predetermined cut-off value. Treating breast cancer comprises administering a composition comprising breast tumour proteins and nucleic acids, which simulates and/or expands T cells specific for the tumour protein. The present sequence was used to illustrate the invention.

Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 9; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	158
DB	42	CAGGGGAGCGGCAAGAGCAAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	101
QY	159	GACGCTTGGGAGCAAGAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	218
DB	102	GACGCTTGGGAGCAAGAGTGGGCACTCTGGAGACACAAACACTCTCTGTGAA	161


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QY 219 CGCAAGAGCAACGCTGGCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCAG 278
|
|
|
Db 162 CGGCAAGAGCAACGCTGCTCGCTTGGGAGACTACGATGACAGCGCTTTCATGGATCCAG 221
|
|
|
QY 279 GTACCCAGCTCCATGGAGAGATCTGGACAAGCTCCAGAGCTGCTGGTGGGTAAAGT 338
|
|
|
Db 222 GTACCCAGCTCCATGGAGAGATCTGGACAAGCTCCAGAGCTGCTGGTGGGTAAAGT 281
|
|
|
QY 339 CCCGAGAGAGATCTCATCGTCAFGCTCAGGACACTGATGTGAACAAGAGGACAGCA 396
|
|
|
Db 282 CCCGAGAGAGATCTCATCGTCAFGCTCAGGACACTGATGTGAACAAGAGGACAGCA 341
|
|
|
QY 399 AAGAGAGACTGCTCATCATCTGGCTCTGCCAATGGGAATTCAGAGTACTGAAACTCGT 458
|
|
|
Db 342 AAGAGAGACTGCTCATCATCTGGCTCTGCCAATGGGAATTCAGAGTACTGAAACTCGT 401
|
|
|
QY 459 GCTGACAGAGAGATGTCAACTTAATGTCTTGTGACCAACAAAAGAGGACAGCTCTGACAAA 518
|
|
|
Db 402 GCTGACAGAGAGATGTCAACTTAATGTCTTGTGACCAACAAAAGAGGACAGCTCTGACAAA 461
|
|
|
QY 519 GGCGGTACATGCCAGAGAGATGATGTGGTAAATGCTGTGGAACATGGCATGATCC 578
|
|
|
Db 462 GGCGGTACATGCCAGAGAGATGATGTGGTAAATGCTGTGGAACATGGCATGATCC 521
|
|
|
QY 579 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 638
|
|
|
Db 522 AAATATTCAGATGATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
|
|
|
QY 639 ATTAATGCCAAAAGCACTGCTCTTATACGCTGTGATATGGAATCAAAAACAGCATGG 698
|
|
|
Db 582 ATTAATGCCAAAAGCACTGCTCTTATACGCTGTGATATGGAATCAAAAACAGCATGG 641
|
|
|
QY 699 CCTCACACCTGCTACTGCTGTATACATGACCAAAAACAGCAAGTGTGAAATTTTAAAT 758
|
|
|
Db 642 CCTCACACCTGCTACTGCTGTATACATGACCAAAAACAGCAAGTGTGAAATTTTAAAT 701
|
|
|
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
|
|
|
Db 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 761
|
|
|
QY 819 TGTATGTTGTGATCAGCAAGTATAGTACAGCCCTACTGAGCAAAAATGTTGATGATC 878
|
|
|
Db 762 TGTATGTTGTGATCAGCAAGTATAGTACAGCCCTACTGAGCAAAAATGTTGATGATC 821
|
|
|
QY 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGATGCTGTTTCTAGTCAATCATG 933
|
|
|
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGATGCTGTTTCTAGTCAATCATG 876
|
|
|
RESULT 15
ID ADB13981 standard; cDNA; 879 BP.
XX
AC ADB13981;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA B305 splice variant #11 ORF.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PT 25-FEB-1997; 97US-00806099.
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PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX P-PSDB; ADB13982.
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New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate cancer.

Example 11; Page; 101pp; English.

The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 618 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB13558, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cut-off value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate, and administering the proliferated T cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a known CDNA

CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030185830.

XX
SQ Sequence 879 BP; 263 A; 193 C; 222 G; 201 T; 0 U; 0 Other;

Query Match 78.6%; Score 733; DB 9; Length 879;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	99	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTCTGGAGACCAACAGACTCTCTGTGAA	158
DB	42	CAGGGGAGGGGCAAGAGCAACGTGGGCACCTCTGGAGACCAACAGACTCTCTGTGAA	101
QY	159	GAGCCTTGGGAGCAAGAGTGCAAGTGTCTGCCACTGCTTCCCTCTGTGACAGGGGAG	218
DB	102	GAGCCTTGGGAGCAAGAGTGCAAGTGTCTGCCACTGCTTCCCTCTGTGACAGGGGAG	161
QY	219	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATCAGCGCCTTCATGGATCCCAG	278
DB	162	CGGCAAGAGCAACGTGGGCGCTTGGGAGACTACGATCAGCGCCTTCATGGATCCCAG	221
QY	279	GTACCACTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGT	338
DB	222	GTACCACTCCATGGAGAGATCTGGACAAGCTCCACAGAGCTGCTGTGGGTAAAGT	281
QY	339	CCCAGAAAGATCTCATCTGTCAGGACACTGTGTAACAAGAGGACCAAGCA	398
DB	282	CCCAGAAAGATCTCATCTGTCAGGACACTGTGTAACAAGAGGACCAAGCA	341
QY	399	AAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT	458
DB	342	AAAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGTAAACTCGT	401
QY	459	GCTGGACAGACGATCAACTTAATGCTTGCACAAAAGAGGACGCTCTGACAA	518
DB	402	GCTGGACAGACGATCAACTTAATGCTTGCACAAAAGAGGACGCTCTGACAA	461
QY	519	GGCGGTACAAATCCAGGAAGATGATGCTGTTAATGTTCTGGAACTGGCACTGATCC	578
DB	462	GGCGGTACAAATCCAGGAAGATGATGCTGTTAATGTTCTGGAACTGGCACTGATCC	521
QY	579	AAATATTCAGATGAGTGAATACCACTCTACACTATGCTGTCTACATGAAGATAA	638
DB	522	AAATATTCAGATGAGTGAATACCACTCTACACTATGCTGTCTACATGAAGATAA	581
QY	639	ATTAATGCCAAAGCACTGCTCTTATACGTTGCTGTATCGAATCAAAAACAGCATGG	698
DB	582	ATTAATGCCAAAGCACTGCTCTTATACGTTGCTGTATCGAATCAAAAACAGCATGG	641
QY	699	CCTCACACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT	758
DB	642	CCTCACACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAAAT	701
QY	759	CAAGAAAAGCGAATTTAATGCGTGTGATGATGAGAGACTGCTCTCATCTGTC	818
DB	702	CAAGAAAAGCGAATTTAATGCGTGTGATGATGAGAGACTGCTCTCATCTGTC	761
QY	819	TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC	878
DB	762	TGTATGTTGTGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC	821
QY	879	TTCTCAGATCTGGAAGACGGCCAGAGATGCTGTTTCTAGTCATCATG	933
DB	822	TTCTCAGATCTGGAAGACGGCCAGAGATGCTGTTTCTAGTCATCATG	876

Search completed: April 30, 2004, 14:21:14
Job time : 428 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	733	78.6	879	4	US-09-439-313-531	Sequence 531, App	
2	733	78.6	879	4	US-09-636-215-531	Sequence 531, App	
3	733	78.6	879	4	US-09-685-166A-531	Sequence 531, App	
4	733	78.6	879	4	US-09-429-755-314	Sequence 314, App	
5	733	78.6	1852	4	US-09-439-313-530	Sequence 530, App	
6	733	78.6	1852	4	US-09-636-215-530	Sequence 530, App	
7	733	78.6	1852	4	US-09-685-166A-530	Sequence 530, App	
8	733	78.6	1852	4	US-09-429-755-313	Sequence 313, App	
c 9	646	69.2	1851	3	US-08-991-789A-231	Sequence 291, App	
c 10	646	69.2	1851	4	US-09-439-313-366	Sequence 366, App	
c 11	646	69.2	1851	4	US-09-662-451-291	Sequence 291, App	
c 12	646	69.2	1851	4	US-09-062-451-292	Sequence 292, App	
c 13	646	69.2	1851	4	US-09-352-616A-366	Sequence 366, App	
c 14	646	69.2	1851	4	US-09-389-198-291	Sequence 291, App	
c 15	646	69.2	1851	4	US-09-289-198-292	Sequence 292, App	
c 16	646	69.2	1851	4	US-09-636-215-366	Sequence 366, App	
c 17	646	69.2	1851	4	US-09-685-166A-366	Sequence 366, App	
c 18	646	69.2	1851	4	US-09-429-755-291	Sequence 291, App	
c 19	646	69.2	1851	4	US-09-429-755-292	Sequence 292, App	
20	646	69.2	2184	4	US-09-439-313-370	Sequence 370, App	
21	646	69.2	2184	4	US-09-062-451-296	Sequence 296, App	
22	646	69.2	2184	4	US-09-352-616A-370	Sequence 370, App	
23	646	69.2	2184	4	US-09-289-198-296	Sequence 296, App	
24	646	69.2	2184	4	US-09-636-215-370	Sequence 370, App	
25	646	69.2	2184	4	US-09-685-166A-370	Sequence 370, App	
26	646	69.2	2184	4	US-09-429-755-296	Sequence 296, App	
c 27	366	39.2	454	3	US-08-991-789A-211	Sequence 211, App	

Db 282 CCCGAGAAAGGATCTCATGTCATGTCAGGACACGATGTGAACAGAGGGACACGA 341
Qy 399 AAGAGGACTGCTTACATCTGCGCTCTGCCAATGGAAATCAGAAAGTAGTAAACTCGT 458
Db 342 AAGAGGACTGCTTACATCTGCGCTCTGCCAATGGAAATCAGAAAGTAGTAAACTCGT 401
Qy 459 GCTGGACAGACGATGTCAACTTAATGCTCTGACAAACAAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGACGATGTCAACTTAATGCTCTGACAAACAAAGAGGACAGCTCTGACAAA 461
Qy 519 GCGCGTACAAATGCCAGAAAGATGAATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 578
Db 462 GCGCGTACAAATGCCAGAAAGATGAATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 521
Qy 579 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 538
Db 522 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CCTCACACCACTGCTACTTGGTATATACATGACGCAAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTTGGTATATACATGACGCAAAACAGCAAGTGGTGAATTTTAA 701
Qy 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATATCTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATATCTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATGATGAGCAAAACAGCAAGTGGTGAATTTTAA 878
Db 762 TGTATGTTGGATCAGCAAGTATGATGAGCAAAACAGCAAGTGGTGAATTTTAA 821
Qy 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 2

US-09-636-215-531

; Sequence 531, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 21021.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 952

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 531

; LENGTH: 879

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-531

Query Match

78.8%; Score 733; DB 4; Length 879;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 99 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAAGACTCTCTGTGAA 158
Db 42 CAGGGGAGCGGCAAGAGCAACCTGGGCACTTCTGGAGACCAACAAGACTCTCTGTGAA 101
Qy 159 GACGCTTGGAGACCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 218
Db 102 GACGCTTGGAGACCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 161
Qy 219 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 278
Db 162 CGGCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 221
Qy 279 GTACCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 338
Db 222 GTACCAAGAGCAACCTGGGCGCTTGGGAGACTAGTACAGAGCGCTTCTATGATCCAG 281
Qy 339 CCCAGAAAGGATCTCATCTGTCATGCTCAGGAGCACTGTGTAACAAGAGGACAGCA 398
Db 282 CCCAGAAAGGATCTCATCTGTCATGCTCAGGAGCACTGTGTAACAAGAGGACAGCA 341
Qy 399 AAGAGGACTGCTTACATCTGCGCTTGGCAATGGGAATTCAGAGTAGTAAACTCGT 458
Db 342 AAGAGGACTGCTTACATCTGCGCTTGGCAATGGGAATTCAGAGTAGTAAACTCGT 401
Qy 459 GCTGGACAGACGATGTCACCTTAATGCTTGTGCAACAACAAGAGGACAGCTCTGACAAA 518
Db 402 GCTGGACAGACGATGTCACCTTAATGCTTGTGCAACAACAAGAGGACAGCTCTGACAAA 461
Qy 519 GCGCGTACAAATGCCAGAAAGATGAATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 578
Db 462 GCGCGTACAAATGCCAGAAAGATGAATGTCGTTAATGTTGCTGGAAACATGGCACTGATCC 521
Qy 579 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 638
Db 522 AATATTTCCAGATGAGTATGGAATACCACTCTACACTATGCTCTACAAATGAAGATAA 581
Qy 639 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGGCCAAAGCACTGCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCATGG 641
Qy 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAA 758
Db 642 CCTCACACCACTGCTACTTGGTATACATGAGCAAAACAGCAAGTGGTGAATTTTAA 701
Qy 759 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATATCTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGTGTGATATGGAAGAACTGCTCTCATATCTGC 761
Qy 819 TGTATGTTGGATCAGCAAGTATGATGAGCAAAACAGCAAGTGGTGAATTTTAA 878
Db 762 TGTATGTTGGATCAGCAAGTATGATGAGCAAAACAGCAAGTGGTGAATTTTAA 821
Qy 879 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGACGGCCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 3

US-09-685-166A-531

; Sequence 531, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi


```
QY 579 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAAATGAAGATAA 638
Db 522 AAATATCCAGATGATGGAATACCACTCTACATATGCTGTCTACAAATGAAGATAA 581
QY 639 ATTAATGCCCAAGCACTGCTTTATACGCTGCTGATATGAATCAAAAAACAAGCATGG 698
Db 582 ATTAATGCCCAAGCACTGCTTTATACGCTGCTGATATGAATCAAAAAACAAGCATGG 641
QY 699 CCTCACACCACTGCTTGTATATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 758
Db 642 CCTCACACCACTGCTTGTATATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 701
QY 759 CAAGAAAAAGCGAATTTAAATGCGCTGGATATGGAAGACTGCTCTCATATCTGC 818
Db 702 CAAGAAAAAGCGAATTTAAATGCGCTGGATATGGAAGACTGCTCTCATATCTGC 761
QY 819 TGTATGTTGCGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC 878
Db 762 TGTATGTTGCGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC 821
QY 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 822 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 876

RESULT 5
US-09-439-313-530
; Sequence 530, Application US/09439313
; Patent No. 629505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; TYPE: DNA
; LENGTH: 1852
; ORGANISM: Homo sapiens
US-09-439-313-530

Query Match 78.6%; Score 733; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 158
Db 771 CAGGGAGCGGCAAGAGCAACGTGGGCACTTTGGAGACCAACAGCACTCTCTGTGAA 830
QY 159 GACCTTTGGAGCAAGAGGTCAGTGTGCTGCCACTGCTCCCTGCTGCAAGGGGAG 218
Db 831 GACCTTTGGAGCAAGAGGTCAGTGTGCTGCCACTGCTCCCTGCTGCAAGGGGAG 990
QY 219 CGGCAAGCAACCTGGCGCTTTGGGAGACTACGATCAGCAGGCGCTTCATGATCCCGAG 278
Db 891 CGGCAAGCAACCTGGCGCTTTGGGAGACTACGATCAGCAGGCGCTTCATGATCCCGAG 950
QY 279 GTACCACTCCATGGAAGATCTGGACAGCTCCACAGAGCTGCTGTGGGTTAAAGT 338
Db 951 GTACCACTCCATGGAAGATCTGGACAGCTCCACAGAGCTGCTGTGGGTTAAAGT 1010
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QY 339 CCCGAGAAAGATCTCATCTGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 398
Db 1011 CCCGAGAAAGATCTCATCTGCTCAGGACACTGATGTGAACAAGAGGCAAGCA 1070
QY 399 AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTGGT 458
Db 1071 AAAGAGGACTGCTTACATCTGGCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTGGT 1130
QY 459 GCTGCAGACAGACCATGCTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGCTCTGACAAA 518
Db 1131 GCTGCAGACAGACCATGCTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGCTCTGACAAA 1190
QY 519 GGCCTCATACATGCCAGGAAGATGAGTGGCTTAATGTGCTGGAAACATGGCACTGATCC 578
Db 1191 GGCCTCATACATGCCAGGAAGATGAGTGGCTTAATGTGCTGGAAACATGGCACTGATCC 1250
QY 579 AAATATTCAGATGATGTAATGAAATACCACTCTACACTATGCTCTCAATGAAGATAA 638
Db 1251 AAATATTCAGATGATGTAATGAAATACCACTCTACACTATGCTCTCAATGAAGATAA 1310
QY 639 ATTAATGCCCAAGCACTGCTCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 698
Db 1311 ATTAATGCCCAAGCACTGCTCTTATACGCTGCTGATATCGAATCAAAAAACAAGCATGG 1370
QY 699 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 758
Db 1371 CCTCACACCACTGCTACTTGGTATACATGAGCAAAAAACAGCAAGTGTGAAATTTTAAAT 1430
QY 759 CAAGAAAAAGCGAATTTTAAATGCGCTGGATATGGAAGACTGCTCTCATATCTGC 818
Db 1431 CAAGAAAAAGCGAATTTTAAATGCGCTGGATATGGAAGACTGCTCTCATATCTGC 1490
QY 819 TGTATGTTGCGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC 878
Db 1491 TGTATGTTGCGATCAGCAAGTATAGTCAGCCCTCTACTTGGCAAAATGTTGATGTATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGGCAGAGAGTATGCTGTTTCTAGTCATCATG 1605

RESULT 6
US-09-636-215-530
; Sequence 530, Application US/09636215
; Patent No. 662092
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-530

Query Match      78.6%; Score 733; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
DB 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 830

QY 159 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCGCACTGCTTCCCTGCTGAGGGGGAG 218
DB 831 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCGCACTGCTTCCCTGCTGAGGGGGAG 890

QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACCATGACAGCGCTTCATGGATCCCG 278
DB 891 CGGCAAGAGCAAGTGGTGGTGGTGGGAGACTACCATGACAGCGCTTCATGGATCCCG 950

QY 279 GTACCAAGAGCAAGTGGGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 338
DB 951 GTACCAAGAGCAAGTGGGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 1010

QY 339 CCCGAGAGAGTCTCATGCTCATGCTCAGGAGCACTGATGTGAACAGAGGAGCAAGCA 398
DB 1011 CCCGAGAGAGTCTCATGCTCATGCTCAGGAGCACTGATGTGAACAGAGGAGCAAGCA 1070

QY 399 AAAGAGGAGTCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT 458
DB 1071 AAAGAGGAGTCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT 1130

QY 459 GCTGGAGACAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGCAAGTCTGACAAA 518
DB 1131 GCTGGAGACAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGCAAGTCTGACAAA 1190

QY 519 GGCCTGTACAAATCCAGGAGAGTGAATGTGCGTTAATGTGTGGAACTGGCACTGATCC 578
DB 1191 GGCCTGTACAAATCCAGGAGAGTGAATGTGCGTTAATGTGTGGAACTGGCACTGATCC 1250

QY 579 AAATATTCAGATGAGTATGAAATACCACTCTACATCTGCTGTCTCAATGAAGATAA 638
DB 1251 AAATATTCAGATGAGTATGAAATACCACTCTACATCTGCTGTCTCAATGAAGATAA 1310

QY 639 ATTAATGGCCAAAGCACTCTTATAGCGTCTGATATCGAATCAAAAACAAACATG 698
DB 1311 ATTAATGGCCAAAGCACTCTTATAGCGTCTGATATCGAATCAAAAACAAACATG 1370

QY 699 CCTCACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAA 758
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RESULT 7

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US-09-685-166A-530
; Sequence 530, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

```
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-530
```

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Query Match      78.6%; Score 733; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 158
DB 771 CAGGGGAGCGGCAAGAGCAAGTGGGCACTTCTGGAGACCAACAGCACTCTCTGTGAA 830

QY 159 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCGCACTGCTTCCCTGCTGAGGGGGAG 218
DB 831 GACGCTTGGGAGCAAGAGTGCAGTGGTGTGCGCACTGCTTCCCTGCTGAGGGGGAG 890

QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACCATGACAGCGCTTCATGGATCCCG 278
DB 891 CGGCAAGAGCAAGTGGTGGTGGTGGGAGACTACCATGACAGCGCTTCATGGATCCCG 950

QY 279 GTACCAAGAGCAAGTGGGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 338
DB 951 GTACCAAGAGCAAGTGGGAGAGTCTGGCAAGCTCCACAGAGCTGCTGGTGGGTAAGT 1010

QY 339 CCCGAGAGAGTCTCATGCTCATGCTCAGGAGCACTGATGTGAACAGAGGAGCAAGCA 398
DB 1011 CCCGAGAGAGTCTCATGCTCATGCTCAGGAGCACTGATGTGAACAGAGGAGCAAGCA 1070

QY 399 AAAGAGGAGTCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT 458
DB 1071 AAAGAGGAGTCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGT 1130

QY 459 GCTGGAGACAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGCAAGTCTGACAAA 518
DB 1131 GCTGGAGACAGATGTCACCTTAATGTCTTGACAAACAAAGAGAGCAAGTCTGACAAA 1190

QY 519 GGCCTGTACAAATCCAGGAGAGTGAATGTGCGTTAATGTGTGGAACTGGCACTGATCC 578
DB 1191 GGCCTGTACAAATCCAGGAGAGTGAATGTGCGTTAATGTGTGGAACTGGCACTGATCC 1250

QY 579 AAATATTCAGATGAGTATGAAATACCACTCTACATCTGCTGTCTCAATGAAGATAA 638
DB 1251 AAATATTCAGATGAGTATGAAATACCACTCTACATCTGCTGTCTCAATGAAGATAA 1310

QY 639 ATTAATGGCCAAAGCACTCTTATAGCGTCTGATATCGAATCAAAAACAAACATG 698
DB 1311 ATTAATGGCCAAAGCACTCTTATAGCGTCTGATATCGAATCAAAAACAAACATG 1370

QY 699 CCTCACCACTGCTACTTGTGTATACATGAGCAAAAACAGCAAGTGTGAAATTTTAA 758
```

Db 1371 CCTCACACCTGCTACTTGGTATACATAGCAAAACAGCAAGTGGTGAATTTTAAAT 1430
QY 759 CAGAGAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 1431 CAAGAAAGAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 1490
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTACAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
Db 1491 TGTATGTTGTGGATCAGCAAGTATAGTACAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 1605

RESULT 8
US-09-429-755-313
; Sequence 313, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 313
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-429-755-313

Query Match 78.6%; Score 733; DB 4; Length 1852;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 CAGGGGAGGGGCAAGAGCAAGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 158
Db 771 CAGGGGAGGGGCAAGAGCAAGTGGGCACTTCTGGAGACCAAGCACTCTCTGTGAA 830
QY 159 GACCTTTGGGAGCAAGAGTGCAAGTGTGCTGCCACTGCTTCCCTGCTGCGAGGGGAG 218
Db 831 GACCTTTGGGAGCAAGAGTGCAAGTGTGCTGCCACTGCTTCCCTGCTGCGAGGGGAG 890
QY 219 CGGCAAGCAAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG 278
Db 891 CGGCAAGCAAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAG 950
QY 279 GTACCAAGCTCCATGGAGAAGATCGGACAGCTCCACAGAGCTGCTGTTGGGGTAAAGT 338
Db 951 GTACCAAGCTCCATGGAGAAGATCGGACAGCTCCACAGAGCTGCTGTTGGGGTAAAGT 1010
QY 339 CCCAGAGAGAGTCTCATGCTGATGCTCAGGAGCACTGATGGAACAAGAGGACAGCA 398
Db 1011 CCCAGAGAGAGTCTCATGCTGATGCTCAGGAGCACTGATGGAACAAGAGGAGCAAGCA 1070
QY 399 AAAGAGAGCTGCTCTACATCTGGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 458
Db 1071 AAAGAGAGCTGCTCTACATCTGGCCCTCTGCCAATGGGAATTCAGAAGTAGTAAACTCGT 1130
QY 459 GCTGGAGAGAGTCTCACTTAATGCTTGTGCAACAACAAAGAGAGAGAGCTCTGACAAA 519
Db 1131 GCTGGAGAGAGTCTCACTTAATGCTTGTGCAACAACAAAGAGAGAGAGAGCTCTGACAAA 1190
QY 519 GGCCGTACATGCGGAGAGAGTAAATGCTGTTGTAACATGGCACTGATCC 578

Db 1191 GGCCGTACATGCGGAGAGAGTAAATGCTGTTGTAACATGGCACTGATCC 1250
QY 579 AAATATTCAGATAGTATGGAATACCACTTCTACACTATGCTGTCTCAATGAGATAA 638
Db 1251 AAATATTCAGATAGTATGGAATACCACTTCTACACTATGCTGTCTCAATGAGATAA 1310
QY 639 ATTAATGGCCAAAGCACTGCTTATACGGTCTGATATCGAATCAAAACCAAGCATGG 698
Db 1311 ATTAATGGCCAAAGCACTGCTTATACGGTCTGATATCGAATCAAAACCAAGCATGG 1370
QY 699 CTTCAACACACTGCTTACTTGTGATATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 758
Db 1371 CTTCAACACACTGCTTACTTGTGATATGAGCAAAACAGCAAGTGGTGAATTTTAAAT 1430
QY 759 CAAGAAAGAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 818
Db 1431 CAAGAAAGAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCATCTTGC 1490
QY 819 TGTATGTTGTGGATCAGCAAGTATAGTACAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 878
Db 1491 TGTATGTTGTGGATCAGCAAGTATAGTACAGCCCTCTACTTTGAGCAAAATGTTGATGTATC 1550
QY 879 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 1551 TTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 1605

RESULT 9
US-08-991-789A-291/c
; Sequence 291, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 291:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 291:
US-08-991-789A-291

Query Match 69.2%; Score 646; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAAGTACACGCTCCATGAGA 296
Db 944 CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAAGTACACGCTCCATGAGA 885
QY 297 AGATCTGGCAAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAGGATCTCAT 356
Db 884 AGATCTGGCAAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAGGATCTCAT 825
QY 357 CGTCATGCTCAGGAGCACTGATGTGAACAAGAGGCAACAAGAGAGGAGCTGCTTACA 416
Db 824 CGTCATGCTCAGGAGCACTGATGTGAACAAGAGGCAACAAGAGAGGAGCTGCTTACA 765
QY 417 TCTGGCCTCTGCCAATGGGAATTCAGAACTGTAAGTGTAAACTCGTCTGGACAGCATGTCA 476
Db 764 TCTGGCCTCTGCCAATGGGAATTCAGAACTGTAAGTGTAAACTCGTCTGGACAGCATGTCA 705
QY 477 ACTTAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGA 536
Db 704 ACTTAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGA 645
QY 537 AGATGAATGCGGTTAATGTTGCTGGACATGCGCACTGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGCGGTTAATGTTGCTGGACATGCGCACTGATCCAAATATTCAGATGAGTA 585
QY 597 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGGCCAAAGCACT 525
QY 657 GCTCTTATACGGTGTGATGGAATCAAAACAAAGCACTGGCTCTCACCACTGCTACT 716
Db 524 GCTCTTATACGGTGTGATGGAATCAAAACAAAGCACTGGCTCTCACCACTGCTACT 465
QY 717 TGGTATACATGAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 836
Db 404 AAATGGCGTGGATAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 345
QY 837 AAGTATAGTACGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 285

RESULT 10

US-09-439-313-366/c
; Sequence 366, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-366

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAAGTACACGCTCCATGAGA 296
Db 944 CGCTTGGGAGACTACGATGACAGCGCCTTCATGGATCCCAAGTACACGCTCCATGAGA 885
QY 297 AGATCTGGCAAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAGGATCTCAT 356
Db 884 AGATCTGGCAAGCTCCACAGAGCTGCTGCTGGGTAAGTCCCAAGAGGATCTCAT 825
QY 357 CGTCATGCTCAGGAGCACTGATGTGAACAAGAGGCAACAAGAGAGGAGCTGCTTACA 416
Db 824 CGTCATGCTCAGGAGCACTGATGTGAACAAGAGGCAACAAGAGAGGAGCTGCTTACA 765
QY 417 TCTGGCCTCTGCCAATGGGAATTCAGAACTGTAAGTGTAAACTCGTCTGGACAGCATGTCA 476
Db 764 TCTGGCCTCTGCCAATGGGAATTCAGAACTGTAAGTGTAAACTCGTCTGGACAGCATGTCA 705
QY 477 ACTTAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGA 536
Db 704 ACTTAATGCTCTGACACAAAGAGAGGACAGCTCTGACAAAGGCGGTACAAATGCCAGGA 645
QY 537 AGATGAATGCGGTTAATGTTGCTGGACATGCGCACTGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGCGGTTAATGTTGCTGGACATGCGCACTGATCCAAATATTCAGATGAGTA 585
QY 597 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTGCTCAATGAAGATAAATTAATGGCCAAAGCACT 525
QY 657 GCTCTTATACGGTGTGATGGAATCAAAACAAAGCACTGGCTCTCACCACTGCTACT 716
Db 524 GCTCTTATACGGTGTGATGGAATCAAAACAAAGCACTGGCTCTCACCACTGCTACT 465
QY 717 TGGTATACATGAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 836
Db 464 TGGTATACATGAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 405
QY 777 AAATGGCGTGGATAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 836
Db 404 AAATGGCGTGGATAGATGGAAGAACTGCTCTCATATCTTCTGCTATGTTGTGATCAGC 345
QY 837 AAGTATAGTACGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCCCTCTACTTGAGCAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 285
QY 897 ACGGCCAGAGATGCTGTTTCTAGTCATCATCATG 933
Db 284 ACGGCCAGAGATGCTGTTTCTAGTCATCATCATG 248

RESULT 11

US-09-062-451-291/c
; Sequence 291, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-291

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACACGCGCTTCATGGATCCAGTACACGTCATGAGA 296
DB 944 CGCTTGGGAGACTACGATGACACGCGCTTCATGGATCCAGTACACGTCATGAGA 885

QY 297 AGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 356
DB 884 AGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 825

QY 357 CGTCATGCTCAGGACACTGATGTGAACAGAGGACAGCAAGCAAGAGGACTGCTCTACA 416
DB 824 CGTCATGCTCAGGACACTGATGTGAACAGAGGACAGCAAGCAAGAGGACTGCTCTACA 765

QY 417 TCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGTCTGGACAGAGCATGTCA 476
DB 764 TCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGTCTGGACAGAGCATGTCA 705

QY 597 TGGAAATACCACTACACTGCTCTACATGAAGTAAATTTAATCAAGAAAAAGCGAATTT 656
DB 584 TGGAAATACCACTACACTGCTCTACATGAAGTAAATTTAATCAAGAAAAAGCGAATTT 525

QY 657 GCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCAATGGCTCAGCACTGCTACT 716
DB 524 GCTCTTATACGGTGTGATATCGAATCAAAAAACAAGCAATGGCTCAGCACTGCTACT 465

QY 717 TGGTATACATGACAAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 776
DB 464 TGGTATACATGACAAAAACAAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCGAATTT 405

QY 777 AAATGGCTGGATAGATATGGAAGACTGCTCTCATACTTGGTATGTTGGGATCAGC 836
DB 404 AAATGGCTGGATAGATATGGAAGACTGCTCTCATACTTGGTATGTTGGGATCAGC 345

QY 837 AAGTATAGTCAGCCCTCTACTTGGACAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 896

DB 344 AAGTATAGTCAGCCCTCTACTTGGACAAAATGTTGATGTATCTTCTCAAGATCTGGAAG 285

QY 897 ACGGCCACAGAGTATGCTGTTTCTAGTCATCATCATG 933

DB 284 ACGGCCACAGAGTATGCTGTTTCTAGTCATCATCATG 248

RESULT 12
US-09-062-451-292/c
Sequence 292, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-292

Query Match 69.2%; Score 646; DB 4; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 237 CGCTTGGGAGACTACGATGACACGCGCTTCATGGATCCAGTACACGTCATGAGA 296
DB 944 CGCTTGGGAGACTACGATGACACGCGCTTCATGGATCCAGTACACGTCATGAGA 885

QY 297 AGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 356
DB 884 AGATCTGGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCAT 825

QY 357 CGTCATGCTCAGGACACTGATGTGAACAGAGGACAGCAAGCAAGAGGACTGCTCTACA 416
DB 824 CGTCATGCTCAGGACACTGATGTGAACAGAGGACAGCAAGCAAGAGGACTGCTCTACA 765

QY 417 TCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGTCTGGACAGAGCATGTCA 476
DB 764 TCTGGCCTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCGTCTGGACAGAGCATGTCA 705

QY 477 ACTTAATGCTCTGCAACAAAAAGAGGACAGCTCTGCAAAAAGGCCCTACAATGCCAGGA 536
DB 704 ACTTAATGCTCTGCAACAAAAAGAGGACAGCTCTGCAAAAAGGCCCTACAATGCCAGGA 645

Db 944 CGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCGAGTACACGTCATCGAGA 885
Qy 297 AGATCTGGAAGAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGGATCTCAT 356
Db 884 AGATCTGGAAGAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGGATCTCAT 825
Qy 357 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGAGCAAGCAAAAGAGGACTCTCTACA 416
Db 824 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGAGCAAGCAAAAGAGGACTCTCTACA 765
Qy 417 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCCGAAGGATCTCTACA 476
Db 764 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCCGAAGGATCTCTACA 705
Qy 477 ACTTAATGTCTTGAACAACAAAAGAGAGCAGCTCTGACAAAGGCGGTCAAAATGCCAGGA 536
Db 704 ACTTAATGTCTTGAACAACAAAAGAGAGCAGCTCTGACAAAGGCGGTCAAAATGCCAGGA 645
Qy 537 AGATGAATGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGAGTA 585
Qy 597 TGGAAATACCACTCTACACTATGCTCTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTCTCAATGAAGATAAATTAATGGCCAAAGCACT 525
Qy 657 GCTCTTATACGGTGTGATGATGGAATCAAAAACAAAGCATGGCTCTACACCACTGCTACT 716
Db 524 GCTCTTATACGGTGTGATGATGGAATCAAAAACAAAGCATGGCTCTACACCACTGCTACT 465
Qy 717 TGGTATACATGAGCAAAACAGCAGAGTGGTGAATTTTAAATCAAGAAAAGCGAATTT 776
Db 464 TGGTATACATGAGCAAAACAGCAGAGTGGTGAATTTTAAATCAAGAAAAGCGAATTT 405
Qy 777 AAATGCGTGGATAGATGATGGAAGCACTGCTCTCATCTTCTGTATGTTGGATCAGC 836
Db 404 AAATGCGTGGATAGATGATGGAAGCACTGCTCTCATCTTCTGTATGTTGGATCAGC 345
Qy 837 AAGTATAGTACGCTCTACTTGGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCTCTACTTGGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285

RESULT 15

US-09-289-198-292/c
; Sequence 292, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Miser, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01

; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-289-198-292

Query Match 69.2%; Score 646; DB 4; Length 1851;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 237 CGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCGAGTACACGTCATCGAGA 296
Db 944 CGCTTGGGAGACTACGATGACAGCGCTTCTATGATCCCGAGTACACGTCATCGAGA 885
Qy 297 AGATCTGGAAGAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGGATCTCAT 356
Db 884 AGATCTGGAAGAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGGATCTCAT 825
Qy 357 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGAGCAAGCAAAAGAGGACTCTCTACA 416
Db 824 CGTCATGCTCAGGAGACTGATGTGAACAAGAGGAGCAAGCAAAAGAGGACTCTCTACA 765
Qy 417 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCCGAAGGATCTCTACA 476
Db 764 TCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAAGTCCCGAAGGATCTCTACA 705
Qy 477 ACTTAATGTCTTGAACAACAAAAGAGAGCAGCTCTGACAAAGGCGGTCAAAATGCCAGGA 536
Db 704 ACTTAATGTCTTGAACAACAAAAGAGAGCAGCTCTGACAAAGGCGGTCAAAATGCCAGGA 645
Qy 537 AGATGAATGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGAGTA 596
Db 644 AGATGAATGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGAGTA 585
Qy 597 TGGAAATACCACTCTACACTATGCTCTCAATGAAGATAAATTAATGGCCAAAGCACT 656
Db 584 TGGAAATACCACTCTACACTATGCTCTCAATGAAGATAAATTAATGGCCAAAGCACT 525
Qy 657 GCTCTTATACGGTGTGATGATGGAATCAAAAACAAAGCATGGCTCTACACCACTGCTACT 716
Db 524 GCTCTTATACGGTGTGATGATGGAATCAAAAACAAAGCATGGCTCTACACCACTGCTACT 465
Qy 717 TGGTATACATGAGCAAAACAGCAGAGTGGTGAATTTTAAATCAAGAAAAGCGAATTT 776
Db 464 TGGTATACATGAGCAAAACAGCAGAGTGGTGAATTTTAAATCAAGAAAAGCGAATTT 405
Qy 777 AAATGCGTGGATAGATGATGGAAGCACTGCTCTCATCTTCTGTATGTTGGATCAGC 836
Db 404 AAATGCGTGGATAGATGATGGAAGCACTGCTCTCATCTTCTGTATGTTGGATCAGC 345
Qy 837 AAGTATAGTACGCTCTACTTGGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 896
Db 344 AAGTATAGTACGCTCTACTTGGCAAAATGTTGATGATCTTCTCAAGATCTGGAAG 285
Qy 897 ACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 933
Db 284 ACGGCCAGAGAGTATGCTGTTTCTAGTCATCATCATG 248

Search completed: April 30, 2004, 16:07:59
Job time : 99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 14:03:48 ; Search time 2520 Seconds
(without alignments)
11056.117 Million cell updates/sec

Title: US-10-079-137B-343

Perfect score: 933

Sequence: 1 atgggttgaggtaggttc.....tggttcctagtcacatcg 933

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rtd:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	58.0	621	12	BM763942
2	490	52.5	633	12	BM763453
3	177	19.0	865	10	BF676987
4	166	17.8	380	10	BF329652

ALIGNMENTS

RESULT 1	BM763942	621 bp	mRNA	linear	EST 04-MAR-2002				
LOCUS	K-EST0045367	S13KMS5	Homo sapiens	cDNA clone	S13KMS5-25-All 5',				
DEFINITION	mRNA sequence.								
ACCESSION	BM763942	GI:190933557							
VERSION	BM763942.1	EST.							
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
	1 (bases 1 to 621)								
	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,								
	Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and								
	Kim,Y.S.								
TITLE	21C Frontier Korean EST Project 2001								
JOURNAL	Unpublished (2002)								
COMMENT	Genome Research Center								
	Korea Research Institute of Bioscience & Biotechnology								
	52 Eoeun-dong Yuseong-gu, Daefjeon 305-333, South Korea								
	Tel: +82-42-860-4470								
	Fax: +82-42-860-4409								
	Email: yongseung@mail.kribb.re.kr								
	Plate: 25 row: A column: 11								
	High quality sequence stop: 621.								

C	5	97	10.4	607	28	B48260
	6	94	10.1	729	13	BU930826
	7	89	9.5	400	28	AQ141119
	8	74	7.9	505	13	EX492731
	9	71	7.6	894	10	BF675049
C	10	58	6.2	279	12	BI461255
	11	49	5.3	451	9	AI804733
	12	47	5.0	531	28	AQ615477
	13	43	4.6	544	9	AL703938
	14	43	4.6	592	28	AQ372700
	15	39	4.2	187	10	BE089869
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	21	26	2.8	547	13	EX489137
	22	26	2.8	633	13	EX489112
C	23	25	2.7	386	28	AQ134631
C	24	25	2.7	388	28	AQ103336
C	25	22	2.4	245	28	BZ881822
C	26	22	2.4	597	29	CE411112
C	27	21	2.3	365	13	BY776486
C	28	21	2.3	395	13	BY608387
	29	21	2.3	522	28	BZ909892
	30	21	2.3	650	14	CA172232
	31	21	2.3	967	13	BQ959046
	32	21	2.3	1141	10	BF682893
	33	21	2.3	1201	13	BX364413
C	34	20	2.1	152	29	BX895445
	35	20	2.1	240	28	AZ477017
C	36	20	2.1	336	28	AQ697778
	37	20	2.1	488	28	AZ025907
C	38	20	2.1	502	28	AQ596426
	39	20	2.1	646	29	CE329241
C	40	20	2.1	654	13	CA039828
C	41	20	2.1	725	29	CE284133
	42	20	2.1	833	28	BZ442452
	43	20	2.1	853	14	CA757900
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FEATURES
source

Location/Qualifiers
1. .621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="S13KMS5-25-All"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector; PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP), and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 58.0%; Score 541; DB 12; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.1e-279;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 CAAGCAAAAGAGGAGTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAA 452
Db 1 CAAGCAAAAGAGGAGTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAA 60
QY 453 ACTCGTCTGGACAGAGTGTCACTTAAATGTCCTTGACACAAAAGAGGACAGCTCT 512
Db 61 ACTCGTCTGGACAGAGTGTCACTTAAATGTCCTTGACACAAAAGAGGACAGCTCT 120
QY 513 GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC 572
Db 121 GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC 180
QY 573 TGATCCAAATATCCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA 632
Db 181 TGATCCAAATATCCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA 240
QY 633 AGATAAATTAATGCCAAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA 692
Db 241 AGATAAATTAATGCCAAAGACATGCTCTTATACGGTGTGATATCGAATCAAAAACAA 300
QY 693 GCATGGCTCACACCACTGCTTGTGTATACATGACGAAACACAGCAAGTGTGAATTT 752
Db 301 GCATGGCTCACACCACTGCTTGTGTATACATGACGAAACACAGCAAGTGTGAATTT 360
QY 753 TTTAATCAAGAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCAT 812
Db 361 TTTAATCAAGAAAAGCGAATTTAAATGCGCTGGATAGATATGGAAGAACTGCTCTCAT 420
QY 813 ACTTGTGTATGTTGGATCAGCAGATATAGTCAGCCCTTACTTGTGACAAATGTTGA 872
Db 421 ACTTGTGTATGTTGGATCAGCAGATATAGTCAGCCCTTACTTGTGACAAATGTTGA 480
QY 873 TGTATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCAT 932
Db 481 TGTATCTTCTCAAGATCTGGAAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCAT 540
QY 933 G 933
Db 541 G 541

RESULT 2
BM763453

LOCUS
DEFINITION
X-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-All 5', mRNA linear EST 04-MAR-2002
mRNA sequence.
BM763453
BM763453
BM763453.1 GI:19093068
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
Kim,M.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
High quality sequence stop: 633.
Location/Qualifiers
1. .633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="S13KMS5-16-All"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector; PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP), and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

FEATURES
source

Location/Qualifiers
1. .633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="S13KMS5-16-All"
/tissue_type="myeloma"
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/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector; PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP), and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 52.5%; Score 490; DB 12; Length 633;
Best Local Similarity 99.8%; Pred. No. 6.1e-252;
Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 CAAGCAAAAGAGGAGTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAA 452
Db 1 CAAGCAAAAGAGGAGTCTCTACATCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAA 60
QY 453 ACTCGTCTGGACAGAGTGTCACTTAAATGTCCTTGACACAAAAGAGGACAGCTCT 512
Db 61 ACTCGTCTGGACAGAGTGTCACTTAAATGTCCTTGACACAAAAGAGGACAGCTCT 120
QY 513 GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC 572
Db 121 GACAAAGCCGTACAATGCCAGGAGATGAATGTGGTTAATGTTCTGGACATGGCAC 180
QY 573 TGATCCAAATATCCAGATGAGTATGAAATACCACTTACACTATGCTGTCTACAAATGA 632

Db 181 TGATCCAAATATTCAGATGAGTATGGAATACCACTTACACTATGCTGTTCAATGA 240

QY 633 AGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAA 692

Db 241 AGATAAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAATCAAAAACAA 300

QY 693 CGATGGCTCACAACCACTGCTACTTGTATATACATGAGCAAAAACAGCAAGTGGTGAAT 752

Db 301 CGATGGCTCACAACCACTGCTACTTGTATATACATGAGCAAAAACAGCAAGTGGTGAAT 360

QY 753 TTTAATCAAGAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGCACTGCTCAT 812

Db 361 TTTAATCAAGAAAAGCAATTTAAATGCGCTGGATAGATATGGAAGCACTGCTCAT 420

QY 813 ACTTCTGTATGTTGTGATCAGCAAGTATATAGTACAGCCCTTACTTGAAGCAAAATGTGA 872

Db 421 ACTTCTGTATGTTGTGATCAGCAAGTATATAGTACAGCCCTTACTTGAAGCAAAATGTGA 480

QY 873 TGTATCTTCTCAAGATCTGGAAGACGCGCAGAGATATGTTCTTGTAGTCATCAT 932

Db 481 TGTATCTTCTCAAGATCTGGAAGACGCGCAGAGATATGTTCTTGTAGTCATCAT 540

QY 933 G 933

Db 541 G 541

RESULT 3

BF676987

LOCUS 602084215F1 NIH_MGC_83 865 bp mRNA linear EST 21-DEC-2000

DEFINITION 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5', mRNA sequence.

ACCESSION BF676987

VERSION BF676987.1 GI:11950882

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 865)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LCM1067 row: m column: 03

High quality sequence stop: 642.

Location/Qualifiers

FEATURES

source

1..865

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4248746"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGCGCGAGCGCCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 19.0%; Score 177; DB 10; Length 865;

Best Local Similarity 99.6%; Pred. No. 2e-83;

Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 174 TCTACATGAAGATAAATTAATTAATGCGCAAGCACTGCTCTTATACGGTCTGATATCGAAT 233

QY 683 CAAAAACAAGATGCGCTCACAACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAG 742

Db 234 CAAAAACAAGATGCGCTCACAACCACTGCTACTTGGTATACATGAGCAAAAACAGCAAG 293

QY 743 TGGTGAATTTTAAATCAAGAAAAGCAATTTAAATGCGCTGATATGGAAGAA 802

Db 294 TGGTGAATTTTAAATCAAGAAAAGCAATTTAAATGCGCTGATATGGAAGAA 353

QY 803 CTCTCTCTCATCTTGTCTGTATGTTGGATCAGCAAGTATAGTCAGCC 850

Db 354 CTCTCTCTCATCTTGTCTGTATGTTGGATCAGCAAGTATAGTCAGCC 401

RESULT 4

BF329652/c

LOCUS BF329652 380 bp mRNA linear EST 22-NOV-2000

DEFINITION RC6-BN0276-160600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF329652

VERSION BF329652.1 GI:11300400

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 380)

AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC6&t2=RC6-BN0276-160600-011-F12&t3=2000-06-16&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 99

High quality sequence stop: 379.

Location/Qualifiers

FEATURES

source

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/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BN0276"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

ORIGIN
Query Match      17.8%; Score 166; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.4e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 CAGGGGAGCGGAGAGCAAGTGGGCACTTGTGGAGACACAAACGACTCCTCTGTGAA 158
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QY 159 GACGCTTGGGAGCAAGAGTGCAGTGTGCTGCCACTGTTCCTCCCTGCTGCAGGGGAG 218
Db 222 GACGCTTGGGAGCAAGAGTGCAGTGTGCTGCCACTGTTCCTCCCTGCTGCAGGGGAG 163
QY 219 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCC 264
Db 162 CGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGCGCC 117

RESULT 5
B48260/c
LOCUS
DEFINITION B48260 607 bp DNA linear GSS 08-APR-1999
            RPC111-6K4.TV RPC111 Homo sapiens genomic clone RPC111-6K4,
            genomic survey sequence.
ACCESSION B48260
VERSION B48260.1 GI:2600497
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 607)
            Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
            Golden,K., Berry,K., Granger,D., Sub,E., Wible,C., de Jong,P. and
            Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: madamsm@igrr.org
            Clones are derived from the human BAC library RPC111. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.
FEATURES
            Location/Qualifiers
            source          1..607
                        /organism="Homo sapiens"
                        /mol_type="Genomic DNA"
                        /db_xref="GDB:7502163"
                        /db_xref="taxon:9606"
                        /clones="RPC111-6K4"
                        /sex="Male"
                        /cell_type="Lymphocytes"
                        /clone_lib="RPC111"
                        /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
                        RPC111 Human Male BAC Library"

ORIGIN
Query Match      10.4%; Score 97; DB 28; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 TCTGCCAATGGGAATTCAGAGTAGTAAACTCGTGGACAGACGATGTCAACTTAAT 483

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Db 182 TCTGCCAATGGGAATTCAGAGTAGTAAACTCGTGGACAGACGATGTCAACTTAAT 123
QY 484 GTCCCTTGACACAAAAGAGGACAGCTCTGACAAAGG 520
Db 122 GTCCCTTGACACAAAAGAGGACAGCTCTGACAAAGG 86

RESULT 6
B4930826
LOCUS
DEFINITION B4930826 729 bp mRNA linear EST 18-OCT-2002
            AGENCOURT 10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
            5', mRNA sequence.
ACCESSION B4930826
VERSION B4930826.1 GI:24119645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 729)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILLNL at:
            http://image.llnl.gov
            Plate: LLCW2943 row: O column: 04
            High quality sequence stop: 555.
FEATURES
            Location/Qualifiers
            source          1..729
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:6668956"
                        /lab_host="DH10B (T1 phage-resistant)"
                        /clone_lib="NIH_MGC_83"
                        /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                        Site 1: SfII (ggcgctcgccg); Site 2: SfiI
                        (ggcattatggcc); 5' and 3' adaptors were used in cloning
                        as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
                        and 3' adaptor sequence:
                        5'-ATTCTAGAGCGCGGCGCGGCGGACATG-dt(30)BN-3' (where B = A,
                        C, or G and N = A, C, G, or T). Average insert size 1.4
                        Kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
                        by PCR. This library was enriched for full-length clones
                        and was constructed by Clontech Laboratories (Palo Alto,
                        CA)."

ORIGIN
Query Match      10.1%; Score 94; DB 13; Length 729;
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 AGGCGGTACAATGCCAGGAAGATGTCGTTAATGTTCTGCGAATGCGCACTGATC 577
Db 89 AGGCGGTACAATGCCAGGAAGATGTCGTTAATGTTCTGCGAATGCGCACTGATC 148
QY 578 CAAATATTCGAGTGAATGATGAAATACCACTCT 611
Db 149 CAAATATTCGAGTGAATGATGAAATACCACTCT 182

RESULT 7
AQ124119
LOCUS
DEFINITION HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens
            AQ124119
            400 bp DNA linear GSS 22-SEP-1998
            HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens

```


sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey sequence.									
ACCESSION	AQ124119								
VERSION	AQ124119.1 GI:3501285								
KEYWORDS	GSS.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Fuzlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.								
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)								
MEDLINE	99380589								
PUBMED	10449764								
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3122 row: E column: 13 Class: BAC ends High quality sequence stop: 400.								
FEATURES	Location/Qualifiers								
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	/sex="male"								
	/clone_lib="CIR Approved Human Genomic Sperm Library D"								
	/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"								
ORIGIN									
Query Match	9.5%; Score 89; DB 28; Length 400;								
Best Local Similarity	100.0%; Pred. No. 4.1e-36;								
Matches	89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY	518 AGCCCGTACAAATGCCAGGAAGATGATGTCGGTTAATGTTGCTGGAAACATGGCACTGATC 577								
Db	237 AGCCCGTACAAATGCCAGGAAGATGATGTCGGTTAATGTTGCTGGAAACATGGCACTGATC 296								
QY	578 CAAATATTCAGATGAGTATGGAAATACC 606								
Db	297 CAAATATTCAGATGAGTATGGAAATACC 325								
RESULT 8									
EX492731									
LOCUS	BX492731								
DEFINITION	DKFZP781C0523 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone								
ACCESSION	DKFZP781C0523-5', mRNA sequence.								
VERSION	BX492731								
KEYWORDS	BX492731.1 GI:32004516								
SOURCE	EST.								
ORGANISM	Homo sapiens (human)								
REFERENCE	Homo sapiens								
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
1	(bases 1 to 505)								
REFERENCE	Bloecker,H., Boecker,M., Meves,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Had,M. and Wiemann,S.								
TITLE	EST (Bloecker,H., Boecker,M., Meves,H.W., Weil,B., Amid,C., et al.)								
JOURNAL	Unpublished (2003)								
COMMENT	Contact: MIPS								
	MIPS								

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: Sfil (ggcgcctggcc); Site 2: Sfil (ggccattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 7.6%; Score 71; DB 10; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2.3e-26;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 TCTACATGAGATAAATTAATGCGCAAGCACTGCTTATACGTCGTGATCGAAT 682
 Db 135 TCTACATGAGATAAATTAATGCGCAAGCACTGCTTATACGTCGTGATCGAAT 194

QY 683 CAAAAACAAG 693
 Db 195 CAAAAACAAG 205

RESULT 10

BI461255/c
 LOCUS BI461255 279 bp mRNA linear EST 21-AUG-2001
 DEFINITION 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
 mRNA sequence.

ACCESSION

VERSION BI461255.1 GI:15251911

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 279)
 NIH-MGC http://mgc.nci.nih.gov/

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Teshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM11687 Row: 9 Column: 21

High quality sequence stop: 236.

FEATURES

source

1. 279
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5272364"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.2%; Score 58; DB 12; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ATGCGGCTGCTCTTCTGTGAAGAAGCCATTGCTTCAGAGCAAGTGGCAAGT 79
 Db 63 ATGCGGCTGCTCTTCTGTGAAGAAGCCATTGCTTCAGAGCAAGTGGCAAGT 6

RESULT 11

AI804733

LOCUS

DEFINITION

AI804733 451 bp mRNA linear EST 07-MAR-2000
 tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
 mRNA sequence.

ACCESSION

VERSION AI804733.1 GI:5370205

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 451)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 543 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. 451
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 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

ORIGIN

source

1. 451
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
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 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
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 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

Location/Qualifiers

1. 451
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2253677"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 110192-1101959, and 121728-1220615).
 Subtraction by Bento Soares and M. Fatima Boraldo."

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genomic clone Plate=720 Col=1 Row=N, genomic survey sequence.
ACCESSION AQ615477 GI:5076753
VERSION AQ615477.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 93380589
PUBMED 10449784
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 720 row: N column: 1
Seq primer: T7
Class: BAC ends
High quality sequence stop: 531.
Location/Qualifiers
FEATURES
source
1..531
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/db_xref="taxon:9606"
/clone="Plate=720 Col=1 Row=N"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
ORIGIN
Query Match 5.0%; Score 47; DB 28; Length 531;
Best Local Similarity 100.0%; Pred. NO. 1.7e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 565 CATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 611
Db 117 CATGGCACTGATCCAAATATTCAGATGAGTATGGAATACCACTCT 163
RESULT 13
LOCUS AL703938 544 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686E1728 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
KEYWORDS DKFZp686E1728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
Wiemann,S.

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EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
FEATURES
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1..544
/organism="Homo sapiens"
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/clone_lib="686 (synonym: hlcc3)"
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Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 623 TCTACAATGAAGATAAATAATTAATGCGCAAGCACTGCTCTTATA 665
Db 91 TCTACAATGAAGATAAATAATTAATGCGCAAGCACTGCTCTTATA 133
RESULT 14
LOCUS AQ372700 592 bp DNA linear GSS 20-MAY-1999
DEFINITION RPCI11-14712.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-14712,
genomic survey sequence.
ACCESSION AQ372700
VERSION AQ372700.1 GI:4343723
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI11-14712.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetig@ig.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
FEATURES
source
1..592

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/organism="Homo sapiens"
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RPC111 Human Male BAC Library"

ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 2.5e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 TCTACATGAGTAATAATTAATGCGCAAGCACTGCTCTTATA 665
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Db 148 TCTACATGAGTAATAATTAATGCGCAAGCACTGCTCTTATA 190

RESULT 15
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LOCUS CM1-BT0397-201299-073-all BT0397 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE069869
ACCESSION BE069869
VERSION BE069869.1 GI:8414519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=CM1-BT0397-201
299-073-all&tl3=1999-12-20&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1..187
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 4.2%; Score 39; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. NO. 3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 GATATCGAATCAAAAAACAAGCATGGCGCTCACACCACTG 711
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Db 91 GATATCGAATCAAAAAACAAGCATGGCGCTCACACCACTG 129

Search completed: April 30, 2004, 16:06:11
Job time : 2524 secs